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(54) Title: GENE EXPRESSION PROFILES IN GRANULOCYTIC CELLS

(57) Abstract: The present invention identifies the global changes in gene expression associated with activation of granulocytes. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

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GENE EXPRESSION PROFILES IN GRANULOCYTIC CELLS

RELATED APPLICATION

This application is related to U.S. Provisional Application 60/237,189, filed on October 3, 2000, which is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Granulocytes (*i.e.,* neutrophils, eosinophils and basophils) are involved in the immune response elicited by inflammation and infection. Inflammation is a localized protective response elicited by injury or destruction of tissues which serves to destroy, dilute or wall off both the injurious agent and the injured tissue. It is characterized by fenestration of the microvasculature, leakages of the elements of blood into the interstitial spaces, and migration of leukocytes into the inflamed tissue. On a macroscopic level, this is usually accompanied by the familiar clinical signs of erythema, edema, tenderness (hyperalgesia), and pain. During this complex response, chemical mediators such as histamine, 5-hydroxytryptamine, various chemotactic factors, bradykinin, leukotrienes, and prostaglandins are released locally. Phagocytic cells migrate into the area, and cellular lysosomal membranes may be ruptured, releasing lytic enzymes. All of these events may contribute to the inflammatory response.

Inflammation is initiated by, among other things, trauma, tissue necrosis, infection or immune reactions. The immediate response is temporary vasoconstriction. Vasoconstriction is followed within seconds by the acute vascular response resulting in increased blood flow (hyperemia) and edema. The acute phase is also characterized by the margination of polymorphonuclear white blood cells (neutrophils) next to endothelial cells, followed by emigration of neutrophils into the adjacent tissue. Margination is recognized by the lining up of neutrophils along the endothelium of vessels. Emigration occurs by passage of the inflammatory cells between endothelial cells.

Neutrophils are the first wave of cellular attack on invading organisms and are the characteristic cells of acute inflammation. The appearance of neutrophils in areas of inflammation may be caused by chemicals released from bacteria, factors produced

nonspecifically from necrotic tissue or antibody reacting with antigen. Neutrophils use an actin-rich cytoskeleton to move in a directed manner along a chemotactic gradient from the bloodstream to an inflammatory site where they ingest particles (*e.g,*. bacteria) and immune complexes bearing IgG (via FcR) and/or breakdown products of the complement component C3.

Neutrophils belong to a category of white blood cells known as polymorphonuclear white blood cells. The blood cells with single nuclei (mononuclear cells) form the white blood cell population that includes macrophages, T and B cells. White blood cells that contain segmented nuclei are broadly classified as polymorphonuclear. Polymorphonuclear white blood cells (or "granulocytes") are further subdivided into three major populations on the basis of the staining properties of their cytoplasmic granules in standard hematologic smears or tissue preparations: neutrophils staining pink, eosinophils staining red and basophils staining blue.

Neutrophils (also referred to as polymorphonuclear neutrophils-PMNs) make up 50% to 70% of the white blood cells (WBCs) of the peripheral blood and may be found scattered diffusely in many tissues, although they are most frequently found in areas of acute inflammation or acute necrosis. Like other WBCs, neutrophils are produced from precursor cells in the bone marrow and released into the blood when mature. After entering the circulation, neutrophils are thought to last only 1 or 2 days.

Neutrophils are characterized by numerous cytoplasmic granules that contain highly destructive enzymes that must be kept isolated from the cytoplasm. These granules contain a number of oxygen-independent enzymes as well as oxygen-dependent mechanisms of killing. Upon attraction to sites of inflammation, neutrophils attempt to engulf and digest bacteria coated with antibody and complement. Phagocytosis by neutrophils is also usually accompanied by release of the lysosomal enzymes into the tissue spaces, particularly if the organism is difficult for the neutrophil to digest.

At least three cytoplasmic granules are identifiable in neutrophils: specific granules containing lactoferrin, B cytochrome, the complement receptor CR3 and β_2-integrin; azurophilic granules containing acid hydrolases and other enzymes; and a third granule containing gelatinase.

In addition to the role neutrophils and other granulocytic cells play in immune response to pathogens, including bacterial infection, neutrophils and other granulocytic cells play an unwanted role in many chronic inflammatory diseases. There are many

disease states in which excessive or unregulated granulocytic cell infiltration and activation are implicated in exacerbating and/or causing the disease. For instance, many inflammatory diseases are characterized by massive neutrophil infiltration, such as psoriasis, inflammatory bowel disease, Crohn's disease, asthma, cardiac and renal reperfusion injury, adult respiratory distress syndrome, rheumatoid arthritis, thrombosis and glomerulonephritis. All of these diseases are associated with increased IL-8 production which may be responsible for the chemotaxis of neutrophils into the inflammatory site.

While the role of neutrophil infiltration and activation in inflammation is well known, the biosynthetic responses of neutrophils to pathogens, chemotactic agents, proinflammatory molecules, etc. are not as well understood. Neutrophils were once thought to be in a state of terminal differentiation, thereby lacking biosynthetic ability. This view is consistent with the relative scarcity in mature circulating neutrophils of ribosomes and endoplasmic reticulum and with the ability of neutrophils to ingest particles when RNA and/or protein synthesis has been inhibited. More recently it has been demonstrated that neutrophils perform more active roles in their response to environmental stimuli. Certain of the genes involved in this response have been identified (see Yerramilli, *et al.*, WO 99/10536, specifically incorporated herein by reference).

It has thus recently been established that neutrophils synthesize *de novo* important macromolecules including, but not limited to interleukin (IL) 1, Il-6, Il-8, tumor necrosis factor (TNF), granulocyte and macrophage colony-stimulating factors, interferon (IFN), intercellular adhesion molecule (ICAM-1) and membrane and cytoskeletal molecules, such as major histocompatibility class I antigens and actin (Beaulieu et al (1992) *J. Biolog. Chem.* 267(1):426-432; Arnold *et al.* (1993) *Infect. Immun.* 61(6):2545-2552; and Elsner *et al.* (1995) *Immunobiol* 193:456-464). No study, however, has taken a systematic approach to assess the transcriptional response during neutrophil activation via contact with a pathogen or from neutrophils isolated from a subject with a sterile inflammatory disease.

Eosinophils are another granulocytic or polymorphonuclear white blood cell that are involved in the inflammatory response. Eosinophils are found predominately in two types of inflammation: allergy and parasite infections.

The role of eosinophils in the host response to parasites is thought to be mediated through the components of the eosinophilic granules. Eosinophils are cytotoxic to

schistosome larvae through an antibody-dependent cell-mediated mechanism. Eosinophil cationic proteins are highly toxic for schistosomes and may be responsible for binding of eosinophils to parasitic worms as well as fragmentation of the parasite.

The role of eosinophils in acute inflammation is not fully understood. On one hand, there is evidence that enzymes in eosinophils may serve to limit the extent of inflammation by neutralizing mediators of anaphylaxis, such as LTC4 , histamine and platelet-activating factor. On the other hand, there is increasing evidence that cationic proteins in eosinophilic granules are mediators of acute inflammation. Eosinophil activation is associated with acute tissue injury and cause an intense vasoconstriction in lung microvasculature, followed by increased pulmonary vascular permeability and pulmonary edema.

Basophils or mast cells are the other major cell type characterized as a granulocytic or polymorphonuclear white blood cell. Mast cells contain granules with a variety of biologically active agents which, when released extracellularly (degranulation), cause dilation of the smooth muscle of arterioles (vasodilation), increased blood flow, and contraction of endothelial cells, thereby opening up vessel walls to permit egress of antibodies, complement or inflammatory cells into tissue spaces.

BRIEF SUMMARY OF THE INVENTION

The present invention identifies the global changes in gene expression associated with the activation of granulocytic cells. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. The present inventors have systematically assessed the transcriptional response from granulocytic cells activated through contact with a pathogen or from granulocytic cells isolated from a subject with a sterile inflammatory disease.

In one aspect, the present invention provides a method of detecting granulocyte activation comprising detecting the level of expression in a sample of one or more genes from Tables 2-8 and comparing the expression level to an expression level in an un-activated granulocyte, wherein differential expression of the genes in Tables 2-8 is indicative of granulocyte activation. The present invention also provides a method of modulating granulocyte activation comprising contacting a granulocyte with an agent, wherein the agent alters the expression of at least one gene in Tables 2-8 thereby

modulating granulocyte activation. In a related aspect, the present invention provides a method of screening for an agent capable of modulating granulocyte activation comprising preparing a first gene expression profile of a cell population comprising granulocytes, wherein the expression profile determines the expression level of one or more genes from Tables 2-8, exposing the cell population to the agent, preparing a second gene expression profile of the agent-exposed cell population and comparing the first and second gene expression profiles.

In another aspect, the present invention provides a method of detecting inflamation in a tissue comprising detecting the level of expression in a sample of the tissue of one or more genes from Tables 2-8; wherein the level of expression of the genes in Tables 2-8 is indicative of inflammation. The present invention also provides a method of treating inflammation in a tissue comprising contacting a tissue undergoing n inflammatory response with an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the inflammation. In a related aspect, the present invention provides a method of screening for an agent capable of modulating inflammation in a tissue comprising preparing a first gene expression profile of a sample of the tissue, wherein the expression profile determines the expression level of one or more genes from Tables 2-8, exposing the tissue to the agent, preparing second gene expression profile of the agent-exposed tissue and comparing the first and second gene expression profiles.

In some embodiments, the present invention provides a method of detecting a chronic inflamation in a tissue comprising detecting the level of expression in a sample of the tissue of one or more genes from Tables 2-8, wherein the level of expression of the genes in Tables 2-8 is indicative of a chronic inflammation. The present invention also provides a method of treating a chronic inflammation in a tissue comprising contacting a tissue having a chronic inflammation with an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the chronic inflammation. In a related aspect, the present invention provides a method of screening for an agent capable of modulating a chronic inflammation in a tissue comprising preparing a first gene expression profile of a sample of the tissue, wherein the expression profile determines the expression level of one or more genes from Tables 2-8, exposing the tissue to the agent, preparing second gene expression profile of the agent-exposed tissue and comparing the first and second gene expression profiles.

Some embodiments of the present invention provide a method of detecting an allergic response in a subject comprising obtaining a sample from the subject, the sample comprising granulocytes, preparing a gene expression profile of the sample, wherein the expression profile determines the expression level of one or more genes from Tables 2-8, comparing the expression level to an expression level in a sample from a normal individual, wherein differential expression of the genes in Tables 2-8 is indicative of an allergic response. The invention also provides a method of treating an allergic response in a subject comprising administering to the subject an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the allergic response. In a related embodiment, the present invention provides a method of screening for an agent capable of modulating an allergic response in a subject comprising preparing a first gene expression profile of a sample from the subject wherein the expression profile determines the expression level of one or more genes from Tables 2-8, administering to the subject an agent, preparing a second gene expression profile of a sample from the agent-exposed subject and comparing the first and second gene expression profiles.

In some embodiments, the present invention is a method of detecting exposure of a subject to a pathogen comprising preparing a first gene expression profile of a granulocyte population from the subject wherein the expression profile determines the expression level of one or more genes from Tables 2-8, comparing the first gene expression profile to a second gene expression profile from a granulocyte population exposed to the pathogen and to a third gene expression profile from a granulocyte population not exposed to the pathogen, and determining whether the subject was exposed to the pathogen. In a related embodiment, the invention provides a method of treating a subject exposed to a pathogen comprising administering to the subject an agent, wherein the agent affects the expression of at least one gene in Tables 2-8 thereby treating the subject. In another aspect, the invention provides a method of screening for an agent that modulates a response of a granulocyte population to a pathogen comprising preparing a first gene expression profile of a first sample from the granulocyte population wherein the expression profile determines the expression level of one or more genes from Tables 2-8, exposing a second sample of the granulocyte population to a pathogen and preparing a second gene expression profile from the second sample, contacting the pathogen-exposed granulocyte population with an agent and preparing a third gene expression profile from the agent-contacted pathogen-exposed population, comparing the first, second and third gene

expression profiles and identifying agents that modulate the response of a granulocyte population to the pathogen.

In some embodiments, the present invention provides a method of detecting a sterile inflammatory disease in a subject comprising detecting the level of expression in a sample from the subject of one or more genes from Tables 2-8 wherein the level of expression of the genes in Tables 2-8 is indicative of a sterile inflammatory disease. In another aspect, the present invention provides a method of treating a sterile inflammatory disease in a subject comprising contacting the subject with an agent wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the sterile inflammatory disease. In a related embodiment, the present invention is a method of screening for an agent capable of modulating a sterile inflammatory disease in a subject comprising preparing a first gene expression profile of a sample from the subject wherein the expression profile determines the expression level of one or more genes from Tables 2-8, exposing the subject to the agent, preparing a second gene expression profile of a sample obtained from the agent-exposed subject and comparing the first and second gene expression profiles.

In some preferred embodiments, the present invention provides a composition comprising at least two oligonucleotides wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8. In some preferred embodiments, the invention provides compositions comprising at least 3, 4, 5, 6, 7, 8, 9 or 10 or more oligonucleotides wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8. In some preferred embodiments, at least one oligonucleotide is attached to a solid support which may be a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead, a silica support or any other solid support known to those skilled in the art.

In some aspects, the present invention provides a solid support comprising at least two oligonucleotides wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8. The oligonucleotides may be attached covalently or non-covalently to the solid support and a given support may comprise both covalently attached and non-covalently attached oligonucleotides. The solid supports of the present invention may comprise oligonucleotides attached at varying densities, for example, at least 10 different oligonucleotides may be attached in discrete locations per square centimeter, at least 100 different oligonucleotides may be attached in discrete

locations per square centimeter, at least 1,000 different oligonucleotides may be attached in discrete locations per square centimeter, at least 10,000 different oligonucleotides may be attached in discrete locations per square centimeter.

The present invention also provides a computer system comprising a database containing information identifying an expression level in a cell population comprising granulocytes of a set of genes comprising at least two genes in Tables 2-8 and a user interface to view the information. The computer system of the present invention may further comprise sequence information for the genes and/or information identifying the expression level for the set of genes in a cell population comprising non-activated granulocytes and/or information identifying the expression level of the set of genes in a cell population comprising activated granulocytes. In some preferred embodiments, the computer system of the present invention may comprise records including descriptive information from an external database (for example, GenBank), which information correlates said genes to records in the external database. The present invention also includes methods of using a computer system to present information identifying the expression level in a tissue or cell of at least one gene in Tables 2-8 comprising comparing the expression level of at least one gene in Tables 2-8 in the tissue or cell to the level of expression of the gene in the database. The methods may include comparison of the expression levels of 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more genes in Tables 2-8. In some preferred embodiments, the methods may comprise displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in a cell population comprising activated granulocytes.

The present invention also includes a method of identifying virulence factor genes in a pathogen by preparing a first gene expression profile of a quiescent granulocyte population, preparing a second gene expression profile of a granulocyte population exposed to a virulent or avirulent bacterial strain, preparing a third gene expression profile from a granulocyte population exposed to a bacterial strain with a mutation in a putative bacterial virulence factor gene, comparing the first, second and third gene expression profiles and identifying a bacterial virulence factor gene.

DETAILED DESCRIPTION OF THE INVENTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.*, through control of initiation, provision of RNA

precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. Thus, changes in the expression levels of particular genes (*e.g.*, oncogenes, tumor suppressors, cytokines and the like) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined two sets of cell populations comprising quiescent and activated granulocytes to identify the global changes in gene expression associated with granulocyte, and in particular neutrophil, activation. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Expression profiles of genes in particular tissues, disease states or disease progression stages provide molecular tools for evaluating toxicity, drug efficacy, drug metabolism, development, and disease monitoring. Changes in the expression profile from a baseline profile can be used as an indication of such effects. Those skilled in the art can use any of a variety of known techniques to evaluate the expression of one or more of the genes and/or ESTs identified in the instant application in order to observe changes in the expression profile.

The response of neutrophils to pathogens, including bacterial pathogens, is a subject of primary importance in view of the need to find ways to modulate the immune response to infection. Similarly, the response of neutrophils to agonists (pro-inflammatory molecules) is a subject of primary importance in view of the need to find better ways of controlling inflammation in various disease states. One means of assessing the response of neutrophils to pathogens and agonists is to measure the ability of neutrophils to synthesize specific RNA *de novo* upon contact with the pathogen or agonist.

The following discussion presents a description of the invention as well definitions for certain terms used herein.

Definitions

Granulocytic cells, also known as polymorphonuclear white blood cells, include neutrophils, also known as polymorphonuclear neutrophils or peripheral blood neutrophils, eosinophils, and basophils, also referred to a mast cells.

The term "pathogen" refers to any infectious organism including bacteria, viruses, parasites, mycoplasma, protozoans, and fungi (including molds and yeast). Pathogenic bacteria include, but are not limited to Staphylococci (e.g. aureus), Streptococci (e.g. pneumoniae), Clostridia (e.g. perfringens), Neisseria (e.g. gonorrhoeae), Enterobacteriaceae (e.g. coli as well as Klebsiella, Salmonella, Shigella, Yersinia and Proteus), Helicobacter (e.g. pylori), Vibrio (e.g. cholerae), Campylobacter (e.g. jejuni), Pseudomonas (e.g. aeruginosa), Haemophilus (e.g. influenzae), Bordetella (e.g. pertussis), Mycoplasma (e.g. pneumoniae), Ureaplasma (e.g. urealyticum), Legionella (e.g. pneumophila), Spirochetes (e.g. Treponema, Leptospira and Borrelia), Mycobacteria (e.g. tuberculosis, smegmatis), Actinomyces (e.g. (israelii), Nocardia (e.g. asteroides), Chlamydia (e.g. trachomatis), Rickettsia, Coxiella, Ehrilichia, Rochalimaea, Brucella, Yersinia, Fracisella, and Pasteurella.

The term "sterile inflammatory disease" refers to any inflammatory disease caused by immune or nonimmune mechanisms not directly linked to infection (see Stewart *et al.*). Examples of sterile inflammatory diseases include, but are not limited to psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, cardiac and renal reperfusion injury, thrombosis, adult respiratory distress syndrome, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis and periodontal disease.

The phrase "solid support" refers to any support to which nucleic acids can be bound or immobilized. Preferred solid supports include, but are not limited to, nitrocellulose, nylon, glass, polymeric material, other solid supports which are positively charged and nanochannel glass arrays disclosed by Beattie (WO 95/1175). Solid supports may be in any convenient form including, but not limited to, a membrane, a filter, a tissue culture dish, a strip, a bead and the like.

The phrase "gene expression profile", also referred to as a "differential expression profile" or "expression profile" refers to any representation of the expression of at least one mRNA species in a cell sample or population. A gene expression profile may be used to detect the level of expression of one or more genes of interest. The present invention

provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, *i. e.*, quiescent versus activated. As used herein, the phrase "detecting the level of expression" is seen to include determining whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is seen to be an assay that requires "detecting the level of expression" as that phrase is used herein.

A gene expression profile can refer to an autoradiograph of labeled cDNA fragments produced from total cellular mRNA separated on the basis of size by known procedures. Such procedures include slab gel electrophoresis, capillary gene electrophoresis, high performance liquid chromatography, and the like. Digitized representations of scanned electrophoresis gels are also included as are two and three dimensional representations of the digitized data. A gene expression profile also can be prepared using "DNA chip" technology as described below.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target

gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated. as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.*, probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

The term "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C or T) or modified bases (7-

deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.*, nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity is determined by **BLAST** (**B**asic **L**ocal **A**lignment **S**earch **T**ool) analysis using the algorithm employed by the programs **blastp, blastn, blastx, tblastn** and **tblastx** (Karlin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the **BLAST** program is to

first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.*, (1994) Nature Genet. 6, 119-129) which is fully incorporated by reference. The search parameters for **histogram, descriptions, alignments, expect** (*i.e.*, the statistical significance threshold for reporting matches against database sequences), **cutoff, matrix** and **filter** are at the default settings. The default scoring matrix used by **blastp, blastx, tblastn**, and **tblastx** is the **BLOSUM62** matrix (Henikoff *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89, 10915-10919, fully incorporated by reference). Four **blastn** parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent **Blastp** parameter settings were Q=9; R=2; wink=1; and gapw=32. A **Bestfit** comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

Diagnostic Uses for the Granulocyte Activation Markers

As described herein, the genes and gene expression information provided in Tables 2-8 may be used as diagnostic markers for the prediction or identification of activation state of granulocytes. For instance, a granulocyte-containing sample from a subject may be assayed by any of the methods described herein, and the expression levels from a gene or genes from the Tables, in particular the genes in Tables 2-8, may be compared to the expression levels found in activated and/or quiescent granulocytes. The samples obtained from subjects with a disease affecting granulocyte activation may be compared to similar samples from normal subjects. Differences and/or similarities of the expression profiles may be used to diagnose diseases. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

Use of the Granulocyte Activation Markers for Monitoring Disease Progression

As described herein, the genes and gene expression information provided in Tables 2-8 may also be used as markers for the monitoring of disease progression, for instance, the progress of an infection or a sterile inflammatory disease. For instance, a granulocyte-containing sample from a subject may be assayed by any of the methods described herein, and the expression levels in the sample from a gene or genes from Tables 2-8 may be compared to the expression levels found in activated and/or quiescent granulocytes. Expression profiles generated from a granulocyte-containing sample from normal or diseased subjects may be used, for instance, to monitor disease progression. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

Use of the Granulocyte Activation Markers for Drug Screening

According to the present invention, the genes identified in Tables 2-8 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing an inflammatory response. A candidate drug or agent can be screened for the ability to simulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of drugs' effects by looking at the number of markers which the drugs have and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Agents that are assayed in the methods described herein can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up

these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats

The genes identified as being differentially expressed in quiescent versus activated granulocytes may be used in a variety of nucleic acid detection assays to detect or quantititate the expression level of a gene or multiple genes in a given sample. For example, traditional Northern blotting, nuclease protection, RT-PCR and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention.

Gene expression profiles can be produced by any means known in the art, including, but not limited to the methods disclosed by: Liang *et al.* (1992) *Science* 257:967-971; Ivanova *et al.* (1995) *Nucleic Acids Res.* 23:2954-2958; Guilfoyl *et al.* (1997) *Nucleic Acids Res.* 25(9):1854-1858; Chee *et al.* (1996) *Science* 274:610-614; Velculescu *et al.* (1995) *Science* 270:484-487; Fischer *et al.* (1995) *Proc. Natl. Acad. Sci. USA* 92(12):5331-5335; and Kato (1995) *Nucleic Acids Res.* 23(18):3685-3690. Preferably, gene expression profiles are produced by the methods of Prashar *et al.* (WO 97/05286) and Prashar *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:659-663.

As an example, gene expression profiles as described herein are made to identify one or more genes whose expression levels are modulated in an activated granulocytic cell population such as one exposed to a pathogen or isolated from a subject having a sterile inflammatory disease. The assaying of the modulation of gene expression via the production of a gene expression profile may involve the production of cDNA from polyA RNA (mRNA) isolated from granulocytes as described below .

The mRNAs are isolated from a granulocytic cell source. The cells may be obtained from an *in vivo* source, such as a peripheral blood. As is apparent to one skilled in the art, any granulocytic cell type may be used, however, neutrophils are preferred. Furthermore, the peripheral blood cells that are initially obtained may be subjected to various separation techniques (*e.g.*, flow cytometry, density gradients).

mRNAs are isolated from cells by any one of a variety of techniques. Numerous techniques are well known (*see e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Approach*, Cold Spring harbor Press, NY, 1987; Ausubel et., *Current Protocols in Molecular Biology*, Greene Publishing Co. NY, 1995). In general, these techniques first lyse the cells and then enrich for or purify RNA. In one such protocol, cells are lysed in a Tris-buffered solution containing SDS. The lysate is extracted with phenol/chloroform, and nucleic acids are precipitated. Purification of poly(A)-containing RNA is not a requirement. The mRNAs may, however, be purified from crude preparations of nucleic acids or from total RNA by chromatography, such as binding and elution from oligo(dT)-cellulose or poly(U)-Sepharose®. As stated above, other protocols and methods for isolation of RNAs may be substituted.

The mRNAs are reverse transcribed using an RNA-directed DNA polymerase, such as reverse transcriptase isolated from AMV, MoMuLV or recombinantly produced. Many commercial sources of enzyme are available (*e.g.*, Pharmacia, New England Biolabs, Stratagene Cloning Systems). Suitable buffers., cofactors, and conditions are well known and supplied by manufacturers (*see also*, Sambrook *et al., supra*; Ausubel *et al., supra*).

Various oligonucleotides are used in the production of cDNA. In particular, the methods utilize oligonucleotide primers for cDNA synthesis, adapters, and primers for amplification. Oligonucleotides are generally synthesized as single strands by standard chemistry techniques, including automated synthesis. Oligonucleotides are subsequently de-protected and may be purified by precipitation with ethanol, chromatographed using a sized or reversed-phase column, denaturing polyacrylamide gel electrophoresis, high-pressure liquid chromatography (HPLC), or other suitable method. In addition, within certain preferred embodiments, a functional group, such as biotin, is incorporated. A biotin moiety may be incorporated at any position in the oligonucleotide, for example, at the 5'- or 3'- terminal nucleotide or at internal nucleotide positions. In some embodiments, it may be desirable to incorporate more than one biotin moiety into an oligonucleotide. A biotinylated oligonucleotide may be synthesized using pre-coupled nucleotides, or

alternatively, biotin may be conjugated to the oligonucleotide using standard chemical reactions. Other functional groups, such as florescent dyes, radioactive molecules, digoxigenin, and the like, may also be incorporated.

Partially-double stranded adaptors are formed from single stranded oligonucleotides by annealing complementary single-stranded oligonucleotides that are chemically synthesized or by enzymatic synthesis. Following synthesis of each strand, the two oligonucleotide strands are mixed together in a buffered salt solution (*e.g.*, 1 M NaCl, 100 mM Tris-HCl pH.8.0, 10 mM EDTA) or in a buffered solution containing Mg^{2+} (*e.g.*, 10 mM $MgCl_2$) and annealed by heating to high temperature and slow cooling to room temperature.

The oligonucleotide primer that primes first strand DNA synthesis comprises a 5' sequence incapable of hybridizing to a polyA tail of the mRNAs, and a 3' sequence that hybridizes to a portion of the polyA tail of the mRNAs and at least one non-polyA nucleotide immediately upstream of the polyA tail. The 5' sequence is preferably a sufficient length that can serve as a primer for amplification. The 5' sequence also preferably has an average G+C content and does not contain large palindromic sequence; some palindromes, such as a recognition sequence for a restriction enzyme, may be acceptable. Examples of suitable 5' sequences are CTCTCAAGGATCTACCGCT (SEQ ID No. 1370), CAGGGTAGACGACGCTACGC (SEQ ID No. 1371), and TAATACCGCGCCACATAGCA (SEQ ID No. 1372).

The 5' sequence is joined to a 3' sequence comprising sequence that hybridizes to a portion of the polyA tail of mRNAs and at least one non-polyA nucleotide immediately upstream. Although the polyA-hybridizing sequence is typically a homopolymer of dT or dU, it need only contain a sufficient number of dT or dU bases to hybridize to polyA under the conditions employed. Both oligo-dT and oligo-dU primers have been used and give comparable results. Thus, other bases may be interspersed or concentrated, as long as hybridization is not impeded. Typically, 12 to 18 bases or 12 to 30 bases of dT or dU will be used. However, as one skilled in the art appreciates, the length need only be sufficient to obtain hybridization. The non-polyA nucleotide is A, C, or G, or a nucleotide derivative, such as inosinate. If one non-polyA nucleotide is used, then three oligonucleotide primers are needed to hybridize to all mRNAs. If two non-polyA nucleotides are used, then 12 primers are needed to hybridize to all mRNAs. The 12 primers would have 3'-terminal sequences capable of hybridizing to the two nucleotides

immediately preceding the polyA tail of the mRNA, *i. e.*, would end in AA, AC, AG, AT, CA, CC, CG, CT, GA, GC, GG, or GT. If three non-poly A nucleotides are used then 48 primers are needed (3 X 4 X 4). Although there is no theoretical upper limit on the number of non-polyA nucleotides, practical considerations make the use of one or two non-polyA nucleotides preferable.

For cDNA synthesis, the mRNAs are either subdivided into three (if one non-polyA nucleotide is used) or 12 (if two non-polyA nucleotides are used) fractions, each containing a single oligonucleotide primer, or the primers may be pooled and contacted with a mRNA preparation. Other subdivisions may alternatively be used. Briefly, first strand cDNA is initiated from the oligonucleotide primer by reverse transcriptase (RTase). As noted above, RTase may be obtained from numerous sources and protocols are well known. Second strand synthesis may be performed by RTase (Gubler and Hoffman, *Gene* 25: 263, 1983), which also has a DNA-directed DNA polymerase activity, with or without a specific primer, by DNA polymerase 1 in conjunction with RNaseH and DNA ligase, or other equivalent methods. The double-stranded cDNA is generally treated by phenol:chloroform extraction and ethanol precipitation to remove protein and free nucleotides.

Double-stranded cDNA is subsequently digested with an agent that cleaves in a sequence-specific manner. Such cleaving agents include restriction enzymes. Restriction enzyme digestion is preferred; enzymes that are relatively infrequent cutters (*e.g.*, 5 bp recognition site) are preferred and those that leave overhanging ends are especially preferred. A restriction enzyme with a six base pair recognition site cuts approximately 8% of cDNAs, so that approximately 12 such restriction enzymes should be needed to digest every cDNA at least once. By using 30 restriction enzymes, digestion of every cDNA is assured.

The adapters for use in the present invention are designed such that the two strands are only partially complementary and only one of the nucleic acid strands that the adapter is ligated to can be amplified. Thus, the adapter is partially double-stranded (*i.e.*, comprising two partially hybridized nucleic acid strands), wherein portions of the two strands are non-complementary to each other and portions of the two strands are complementary to each other. Conceptually, the adapter is "Y-shaped" or "bubble-shaped." When the 5' region is non-paired, the 3' end of other strand cannot be extended by a polymerase to make a complementary copy. The ligated adapter can also be blocked

at the 3' end to eliminate extension during subsequent amplifications. Blocking groups include dideoxynucleotides or any other agent capable of blocking the 3'-OH. In this type of adapter ("Y-shaped"), the non-complementary portion of the upper strand of the adapters is preferably a length that can serve as a primer for amplification. As noted above, the non-complementary portion of the lower strand need only be one base, however, a longer sequence is preferable (*e.g.*, 3 to 20 bases; 3 to 15 bases; 5 to 15 bases; or 14 to 24 bases). The complementary portion of the adapter should be long enough to form a duplex under conditions of litigation.

For "bubble-shaped" adapters, the non-complementary portion of the upper strands is preferably a length that can serve as a primer for amplification. Thus, this portion is preferably 15 to 30 bases. Alternatively, the adapter can have a structure similar to the Y-shaped adapter, but has a 3' end that contains a moiety that a DNA polymerase cannot extend from.

Amplification primers are also used in the present invention. Two different amplification steps are performed in the preferred aspect. In the first, the 3' end (referenced to mRNA) of double stranded cDNA that has been cleaved and ligated with an adapter is amplified. For this amplification, either a single primer or a primer pair is used. The sequence of the single primer comprises at least a portion of the 5' sequence of the oligonucleotide primer used for first strand cDNA synthesis. The portion need only be long enough to serve as an amplification primer. the primer pair consists of a first primer whose sequence comprises at least a portion of the 5' sequence of the oligonucleotide primer as described herein; and a second primer whose sequence comprises at least a portion of the sequence of one strand of the adapter in the non-complementary portion. The primer will generally contain all the sequence of the non-complementary potion, but may contain less of the sequence, especially when the non-complementary portion is very long, or more of the sequence, especially when the non-complementary portion is very short. In some embodiments, the primer will contain sequence of the complementary portion, as long as that sequence does not appreciably hybridize to the other strand of the adapter under the amplification conditions employed. for example, in one embodiment, the primer sequence comprises four bases of the complementary region to yield a 19 base primer, and amplification cycles are performed at 56 °C (annealing temperature), 72 °C (extension temperature), and 94 °C (denaturation temperature). In another embodiment, the primer is 25 bases long and has 10 bases of sequence in the complementary portion.

Amplification cycles for this primer are performed at 68 °C (annealing and extension temperature) and 94 °C (denaturation temperature). By using these longer primers, the specificity of priming is increased.

The design of the amplification primers will generally follow well-known guidelines, such as average G-C content, absence of hairpin structures, inability to form primer-dimers and the like. At times, however, it will be recognized that deviations from such guidelines may be appropriate or desirable.

After amplification, the lengths of the amplified fragments are determined. Any procedure that separate nucleic acids on the basis of size and allows detection or identification of the nucleic acids is acceptable. Such procedures include slap get electrophoresis, capillary gel electrophoresis, high performance liquid chromatography, and the like.

Electrophoresis is technique based on the mobility of DNA in an electric flied. Negatively charged DNA migrates towards a positive electrode at a rate dependent on their total charge, size, and shape. Most often, DNA is electrophoresed in agarose or polyacrylamide gels. For maximal resolution, polyacrylamide is preferred and for maximal linearity, a denaturant, such as urea is present. A typical get setup uses a 19:1 mixture of acrylamide:bisacrylamide and a Tris-borate buffer. DNA samples are denatured and applied to the gel, which is usually sandwiched between glass plates. A typical procedure can be found in Sambrook et al (*Molecular Cloning: A Laboratory Approach,* Cold Spring Harbor Press, NY, 1989) or Ausubel *et al.* (*Current Protocols in Molecular Biology,* Greene Publishing Co., NY, 1995). Variations may be substituted as long as sufficient resolution is obtained.

Capillary electrophoresis (CE) in its various manifestations (free solution, isotachophoresis, isoelectric focusing, polyacrylamide get. micellar electrokinetic "chromatography") allows high resolution separation of very small sample volumes. Briefly, in capillary electrophoresis, a neutral coated capillary, such as a 50 μm X 37 cm column (eCAP neutral, Beckman Instruments, CA), is filled with a linear polyacrylamide (*e.g.*, 0.2% polyacrylamide), a sample is introduced by high-pressure injection followed by an injection of running buffer (*e.g.*, 1X TBE). The sample is electrophoresed and fragments are detected. An order of magnitude increase in sensitivity may be achieved with the use of capillary electrophoresis. Capillaries may be used in parallel for increased throughput (Smith *et al.* (1990) *Nuc. Acids. Res.* 18:4417; Mathies and Huang (1992)

Nature 359:167). Because of the small sample volume that can be loaded onto a capillary, a sample may be concentrated to increase level of detection. One means of concentration is sample stacking (Chien and Burgi (1992) *Anal. Chem* 64:489A). In sample stacking, a large volume of sample in a low concentration buffer is introduced to the capillary column. The capillary is then filled with a buffer of the same composition, but at higher concentration, such that when the sample ions reach the capillary buffer with a lower electric field, they stack into a concentrated zone. Sample stacking can increase detection by one to three orders of magnitude. Other methods of concentration, such as isotachophoresis, may also be used.

High-performance liquid chromatography (HPLC) is a chromatographic separations technique that separates compounds in solution. HPLC instruments consist of a reservoir of mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by injecting an aliquot of the sample mixture onto the column. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase. IP-RO-HPLC on non-porous PS/DVB particles with chemically bonded alkyl chains can also be used to analyze nucleic acid molecules on the basis of size (Huber *et al.* (1993) *Anal. Biochem.* 121:351; Huber *et al.* (1993) *Nuc. Acids Res.* 21:1061; Huber *et al.* (1993) *Biotechniques* 16:898).

In each of these analysis techniques, the amplified fragments are detected. A variety of labels can be used to assist in detection. Such labels include, but are not limited to, radioactive molecules (*e.g.*, ^{35}S, ^{32}P, ^{33}P) fluorescent molecules, and mass spectrometric tags. The labels may be attached to the oligonucleotide primers or to nucleotides that are incorporated during DNA synthesis, including amplification.

Radioactive nucleotides may be obtained from commercial sources; radioactive primers may be readily generated by transfer of label from γ-^{32}P-ATP to a 5'-OH group by a kinase (*e.g.*, T4 polynucleotide kinase). Detection systems include autoradiograph, phosphor image analysis and the like.

Fluorescent nucleotides may be obtained from commercial sources (*e.g.*, ABI, Foster city, CA) or generated by chemical reaction using appropriately derivatized dyes. Oligonucleotide primers can be labeled, for example, using succinimidyl esters to conjugate to amine-modified oligonucleotides. A variety of florescent dyes may be used, including 6 carboxyfluorescein, other carboxyfluorescein derivatives, carboxyrhodamine

derivatives, Texas red derivatives, and the like. Detection systems include photomultiplier tubes with appropriate wave-length filters for the dyes used. DNA sequence analysis systems, such as produced by ABI (Foster City, CA), may be used.

After separation of the amplified cDNA fragments, cDNA fragments which correspond to differentially expressed mRNA species are isolated, reamplified and sequenced according to standard procedures. For instance, bands corresponding the cDNA fragments can be cut from the electrophoresis gel, reamplified and subcloned into any available vector, including pCRscript using the PCR script cloning kit (Stratagene). The insert is then sequenced using standard procedures, such as cycle sequencing on an ABI sequencer.

In addition to the methodology described above, gene expression profiles may be prepared using a hybridization assay format. Any hybridization assay format may be used, including solution-based and solid support-based assay formats.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.*, (1996) Nat. Biotechnol. 14, 1675-1680; McGall *et al.*, (1996) Proc. Nat. Acad. Sci. USA 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays may also contain oligonucleotides that are complementary or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70 or more the genes described herein. Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 different nucleic acid hybridizations.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with less processing steps.

The sequences of the expression marker genes are in the public databases, *i. e.*, GenBank. Tables 2-8 provide the GenBank Accession numbers and name for each of the sequences. The sequences of the genes in GenBank have been submitted on an electronic medium in computer readable form in compliance with AI § 801(a) of the PCT and are

expressly incorporated by reference as are identical or related sequences with difference GenBank numbers.

Assays to monitor the expression of a marker or markers as defined in Tables 2-8 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least two genes from Tables 2-8 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, cell lines that contain reporter gene fusions between the open reading frame of a gene in Tables 2-8 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, (1990) Anal. Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 2-8. For instance, as described herein, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to

one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the agent-contacted sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 2-8. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Probe design

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 45 or 5 to about 500 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using natural nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*,

fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the β-actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a twenty-mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For

example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe ($I_{(PM)} - I_{(MM)}$) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, Tijssen, (1993) (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a "clinical sample" which is a sample derived from a subject. In some preferred embodiments, subjects may be mammalian, preferably human. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports

Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc. An solid or semi-solid material conventionally used to immobilize nucleic acids may be used. Solid supports containing oligonucleotide probes for differentially expressed genes

of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc. Such wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000; 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung *et al.*, (1992) U.S. Patent No. 5,143, 854; Fodor *et al.*, (1998) U.S. Patent No. 5,800;992; Chee *et al.*, (1998) 5,837,832

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor *et al.*, (1993). WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade

or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart *et al.*, (1999) WO 99/32660). The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label.

It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6× SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25× SSPET at 37°C to 50°C until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the

hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art (see Lockhart *et al.*, (1999) WO 99/32660).

Databases

The present invention includes relational databases containing sequence information, for instance for the genes of Tables 2-8, as well as gene expression information in various granulocyte-containing samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the subject from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom *et al.*, (1999) U.S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 2-8 the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such has those available from Silicon Graphics. Client-server environments, database servers and

networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northerns to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 2-8 comprising the step of comparing the expression level of at least one gene in Tables 2-8 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of expression of a gene or genes in Tables 2-8 from a sample to the expression levels found in tissue from normal liver, malignant liver or hepatocellular carcinoma. Such methods may also be used in the drug or agent screening assays as described below.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Preparation of Cells

Expression profiles of RNA expression levels from neutrophils exposed to various pathogens, in particular, bacteria offer a powerful means of identifying genes that are specifically regulated in response to infection. As an example, the production of expression profiles from neutrophils exposed to *E. coli* and *Y. pestis* allow the identification of neutrophil genes that are specifically regulated in response to bacterial infection.

Neutrophils may be isolated from normal donor peripheral blood following any protocol known to those skilled in the art. The LPS-free method of isolation is described below. Peripheral blood is isolated using a butterfly needle and a syringe containing 5 cc ACD, 5 cc of 6% Dextran (in normal saline). After 30 minutes of settling, plasma is

collected and HBSS (without Ca^{++} or Mg^{++}) is added to a total volume of 40 ml. The plasma was centrifuged (1500 rpm, for 15 m at 4°C), the supernatant decanted and cold HBSS added to resuspend the cells. The cell suspension was then layered onto a cold Ficoll Hypaq, centrifuged at 500xg for 30m at 4°C. The pellet contains polymorphonuclear neutrophils. Neutrophils can also be isolated by other commonly used methods such as those disclosed in *Current Protocols of Immunology* (John Wiley & Sons, Inc.), Babior *et al.* (1981) In:*Leokocyte Function*, Cline, M.J. Ed., p.1-38 (Church Livingstone, NY), and Haslett *et al.* (1985) *Am. J. Pathol.* 119:101-110.

Following isolation, neutrophils were incubated with *E. coli* or one of three strains of *Y. pestis* ypoH, KIM5 or KIM6 for 30 minutes or two hours and then total RNA was isolated using a standard guanidine•HCl method. Before incubation, bacteria are harvested and washed in phosphate buffered saline and opsonized with either autologous human serum or complement factor C7 deficient human serum (SIGMA). Incubation was at a ratio of approximately a PMN:bacteria ratio of 1:20 in RPMI 1640 (HEPES buffered) with heat inactivated Fetal Bovine Serum at 37°C with gentle mixing in a rotary shaker bath.

As controls, neutrophils were incubated with either bacterial lipopolysaccharide (LPS) or latex beads. LPS was added to approximately 3.38×10^8 cells in 100 ml of RPMI containing 6% autologous serum to a final concentration of 1 ng/ml to 1 µg/l. Incubation proceeded for two hours with gentle rotation in disposable polycarbonate Erlenmeyer flasks at 37°C. After incubation, the cells were spun down and washed once with HBSS and frozen until RNA isolation.

The neutrophils extracted from blood were examined for purity by flow microfluorometry. Preparations with >0.5% monocytes contamination were rejected. Samples of mRNA were later examined for specific expression markers for induced monocytes to bacterial exposure. The neutrophils were cultured with the non-pathogenic bacteria, *E. coli*, or three pathogenic strains of *Yersinia pestis*, KIM5, KIM6, and yopH (Perry *et al.*(1997) Clin. Microbiology Reviews10(1):35-66), respectively, and after 2 hours total RNA was extracted by the standard guanidine•HCl method.

Example 2: Sample Preparation for DNA Chip Analysis

The total RNA was processed for the Affymetrix oligonucleotide GeneChip microarrays following Affmetrix's protocol. The final product, cRNA, was hybridized on

the 42K array set (a combination of the full-length genes and EST's) and the HuGU95A array, containing ~12,000 full length known genes. The data was analyzed to determine present/absent calls, gene expression levels, and expression differences. A gene identified as present or absent has been calculated by an algorithm in the Affymetrix analysis software. Gene expression levels have been measured as average differences. Gene expression changes have been calculated as the ratios of the expressed genes in uninduced/induced neutrophils. Expression differences with a ratio of $\pm \geq 3$ fold have been analyzed.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen cells were first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was 200-500 μg. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 μl, an ethanol precipitation step was required to bring the concentration to 1 μg/μl. Using 1-5 μg of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7-(dT_{24}) oligonucleotide. The cDNA was then phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μg/μl.

From 2 μg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript *in vitro* Transcription Kit. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5× fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

As per the Affymetrix protocol, 55 μg of fragmented cRNA was hybridized on the human 42K set and the HuGU95A array for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major

chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1.0).

All samples were prepared as described and hybridized onto the Affymetrix HuGU95A array, which represents nearly 12,000 full length human genes, and the Human 42K set of arrays (a combination of ESTs and full length genes). Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

Example 3: Gene Expression Analysis

1182 genes have been identified to be present in the uninduced neutrophils. In neutrophils exposed to bacteria, the number of genes present generally decreased. In neutrophils exposed to *E. coli* 819 genes were called present. In neutrophils exposed to *Y. pestis* strain yopH 698 genes were identified and those exposed to strain KIM5 expressed 696 genes. In contrast, neutrophils exposed to KIM6 expresssed 1258 genes (Table 1).

A comparison of the genes called present in the three *Y. pestis* exposed neutrophil populations identified 526 genes as present in all three. 192 genes were switched on or off, with 121 of those with a ratios ≥ 3.

A comparison of all four bacteria-exposed neutrophil populations identified 428 genes that were called present in both *E. coli* and the three *Y. pestis* induced neutrophils.

A number of genes were identified by the comparison of the different induction conditions. Fourteen genes were called absent in uninduced neutrophils and present in all bacteria-exposed neutrophils (Table 2). Twelve genes were called absent in uninduced neutrophils and *E. coli* exposed neutrophils, and present in the three *Y. pestis* strains exposed neutrophils (Table 3) and thus were specifically induced by contact with *Y. pestis*. 135 genes were called absent in uninduced neutrophils, present in *E. coli* exposed neutrophils, and showed variable expression in the three different *Y. pestis* exposed

neutrophils (Table 4).

123 genes were called present in uninduced neutrophils, absent in all bacteria-exposed neutrophils (Table 5).

47 genes were called present in both uninduced neutrophils and bacteria-exposed neutrophils and showed varying expression level in the bacteria-exposed neutrophils. (Table 6).

Analyzing genes that match up in all four induction experiments revealed a set of genes that play an important role in bacterial exposure. Four genes with an increase in expression level in the bacteria-exposed neutrophils have been identified.

TRAF3 (TNF receptor-associated factor 3) has been linked to cell growth and death signal pathways (Mosialos *et al.* (1995) *Cell* 80:389-399). Dual specificity phosphatase 2 (DUSP2) encodes a nuclear protein, PAC1, that is stringent for MAP kinase. MAP phosphorylation and subsequent activation are important for signal transduction of growth factors. DUSP2 down regulates intracellular signal transduction through the dephosphorylation of MAP kinases.

Solute carrier family & (cationic amino acid transporter, y+ system), member 5 (SLC7A5) has been shown to be up regulated in induced myeloid and lymphoid cells, it is a membrane protein connected with membrane transportation (Mastroberardino *et al.* (1998) *Nature* 395:288-91).

GRO2 gene encodes a cytokine involved with inflammatory response and growth regulation (Haskill *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:7732-7736).

Three genes (see Table 3) were up regulated in neutrophils exposed to *Y. pestis* but not in neutrophils exposed to *E. coli* cyclin-dependent kinase inhibitor 1A(p21, Cip1) (CDKN1A), CD44 antigen (CD44) and tumor suppressing subtransferable (TSSC3).

Cyclin-dependent kinase inhibitor 1A(p21, Cip1) (CDKN1A), is an inhibitor of G1 cyclin-dependent kinases (El-Deiry *et al.* (1993) *Cell* 75:817-825).

CD44 antigen (CD44) is up regulated in induced lymphoblastoid cell line, KCA (El-Deiry *et al.* (1993) *Cell* 75:817-825).

Colony stimulating factor 3 (granulocyte) (CSF3) has been identified in haematopoietic cell proliferation and differentation (Dougherty *et al.* (1991) *J. Exp. Med* 174:1-5). Pentaxin-related gene, rapidly induced by IL-1 beta (PTX3) is an inflammatory cytokine identified in stimulated fibroblast cell lines (Souza *et al.* (1986) *Science* 232:61-65).

Nuclear factor (erythroid-derived 2), 45kD (NFE2) has been identified in hematopoietic cell lines (Lee *et al.* (1992) *J. Cell Biol.* 116:545-557). Integrin, beta 2 (antigenCD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2) has been identified with cell surface signaling (Pischedda *et al.* (1995) *Proc. Natl. Acad. Sci.* 92:3511-3515).

A complete list of all genes identified in bacteria-exposed neutrophils is presented in Table 7. The table also provides the ratio of the expression observed in the bacteria-exposed neutrophils to the expression level in quiescent neutrophils.

Genes differentially expressed in quiescent neutrophils as compared to neutrophils exposed to bacteria are genes that are responsive to an induction from various sources. The genes discussed are genes that are specific to cellular induction. Genes not expressed in *E. coli* exposed neutrophils but expressed in *Y. pestis* exposed neutrophils are genes which may make the cell susceptible to infection. The *Y. pestis* bacterium is pathogenic triggering gene expression of genes that inhibit the phagocytic response in neutrophils. Genes expressed in *E. coli* but not in *Y. pestis* exposed neutrophils provide another set of genes that are affected by the pathogenic capacity of *Y. petis*. The genes that were down regulated when neutrophils were exposed to bacteria are genes involved in progression of cell development. One of the many neutrophilic responses to bacteria is the suppression of genes involved in normal cell cycle, this allows the cell to respond to the infection.

The identity of the genes in Tables 2-8 allow one skilled in the art to select an appropriate set of genes in order to assay for exposure to a specific bacterium or strain. In addition those skilled in the art can select an appropriate gene set from the list of affected genes to conduct assays for agents that modulate the activation response of bacteria-exposed neutrophils. Table 1 shows that a large number of genes are affected in a short amount of time (two hours or less). This quick and complex response is consistent to the nature of neutrophils and the expected response *in vivo*. The present invention has identified numerous genes that were not previously known to be involved in the neutrophil response to bacterial contact. The present invention also allows the selection of gene sets specific to different strains of bacteria.

Example 4: Gene Expression Analysis Using Restriction Enzyme Analysis of Differentially Expressed Sequences

Ten micrograms of total RNA, the amount obtainable from about $3x10^6$

neutrophils, is sufficient for a complete set of cDNA expression profiles.

Synthesis of cDNA was performed as previously described by Prashar *et al.* in WO 97/05286 and in Prashar *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:659-663. Briefly, cDNA was synthesized according to the protocol described in the GIBCO/BRL kit for cDNA synthesis. The reaction mixture for first-strand synthesis included 6 μg of total RNA, and 200 ng of a mixture of 1-base anchored oligo(dT) primers with all three possible anchored bases.
(ACGTAATACGACTCACTATAGGGCGAATTGGGTCGACTTTTTTTTTTTTTTTT V wherein V=A or C or G, SEQ ID NO: 1373) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was incubated at 65°C for 5 minutes, chilled on ice and the process repeated. Alternatively, the reaction mixture may include 10μg of total RNA, and 2 pmol of 1 of the 2-base anchored oligo(dT) primers such as RP5.0 (CTCTCAAGGATCTTACCGCT$(T)_{18}$AT, SEQ ID NO: 1374), or RP6.0 (TAATACCGCGCCACATAGCA$(T)_{18}$CG, SEQ ID NO: 1375), or RP9.2 (CAGGGTAGACGACGCTACGC$(T)_{18}$GA, SEQ ID NO: 1376) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was then layered with mineral oil and incubated at 65 °C for 7 min followed by 50 °C for another 7 min. At this stage, 2 μl of Superscript reverse transcriptase (200 units/ μl; GIBCO/BRL) was added quickly and mixed, and the reaction continued for 1 hr at 45-50 °C. Second-strand synthesis was performed at 16 °C for 2 hr. At the end of the reaction, the cDNAs were precipitated with ethanol and the yield of cDNA was calculated. In our experiments, 200 ng of cDNA was obtained from 10 μg of total RNA.

The adapter oligonucleotide sequences were
A1 (TAGCGTCCGGCGCAGCGACGGCCAG, SEQ ID NO: 1377) and
A2 (GATCCTGGCCGTCGGCTGTCTGTCGGCGC, SEQ ID NO: 1378). One microgram of oligonucleotide A2 was first phosphorylated at the 5' end using T4 polynucleotide kinase (PNK). After phosphorylation, PNK was heated denatured, and 1 μg of the oligonucleotide A1 was added along with 10X annealing buffer (1 M NaC1/100 mM Tris-HCl, pH8.0/10 mM EDTA, pH8.0) in a final vol of 20 μl. This mixture was then heated at 65 °C for 10 min followed by slow cooling to room temperature for 30 min, resulting in formation of the Y adapter at a final concentration of 100 ng/ μl. About 20 ng of the cDNA was digested with 4 units of *Bgl* II in a final vol of 10 μl for 30 min at 37 °C. Two microliters (4 ng of digested cDNA) of this reaction mixture was then used for

ligation to 100 ng (50-fold) of the Y-shaped adapter in a final vol of 5 µl for 16 hr at 15 °C. After ligation, the reaction mixture was diluted with water to a final vol of 80 µl (adapter ligated cDNA concentration, 50 pg/µl) and heated at 65 °C for 10 min to denature T4 DNA ligase, and 2 µl aliquots (with 100 pg of cDNA) were used for PCR.

The following sets of primers were used for PCR amplification of the adapter ligated 3'-end cDNAs:

TGAAGCCGAGACGTCGGTCG$(T)_{18}$VN (wherein V = A or C or G, N = A or C or G or T; SEQ ID NO: 1379) as the 3' primer with A1 as the 5' primer or alternatively RP 5.0, RP 6.0, or RP 9.2 were used as 3'- primers with primer A1.1 serving as the 5' primer. To detect the PCR products on the display gel, 24 pmol of oligonucleotide A1 or A1.1 was 5'-end-labeled using 15 µl of [γ -^{32} P]ATP (Amersham; 3000 Ci/mmol) and PNK in a final volume of 20 µl for 30 min at 37 C. After heat denaturing PNK at 65 °C for 20 min, the labeled oligonucleotide was diluted to a final concentration of 2 µM in 80 µl with unlabeled oligonucleotide A1.1. The PCR mixture (20 µl) consisted of 2 µl (100 pg) of the template, 2 µl of 10X PCR buffer (100 mM Tris·HCl, pH 8.3/500 mM KCl), 2 µl of 15 mM $MgCl_2$ to yield 1.5 mM final Mg^{2+} concentration optimum in the reaction mixture, 200 M dNTPs, 200 nM each 5' and 3' PCR primers, and 1 unit of Amplitaq Gold. Primers and dNTPs were added after preheating the reaction mixture containing the rest of the components at 85 °C. This "hot start" PCR was done to avoid amplification artifacts arising out of arbitrary annealing of PCR primers at lower temperature during transition from room temperature to 94 °C in the first PCR cycle. PCR consisted of 5 cycles of 94 °C for 30 sec, 55 °C for 2 min, and 72 °C for 60 sec followed by 25 cycles of 94 °C for 30 sec, 60 °C for 2 min, and 72 °C for 60 sec. A higher number of cycles resulted in smeary gel patterns. PCR products (2.5 µl) were analyzed on 6% polyacrylamide sequencing gel. For double or multiple digestion following adapter ligation, 13.2 µl of the ligated cDNA sample was digested with a secondary restriction enzyme(s) in a final vol of 20 µl. From this solution, 3 µl was used as template for PCR. This template vol of 3 µl carried 100 pg of the cDNA and 10 mM $MgCl_2$ (from the 10X enzyme buffer), which diluted to the optimum of 1.5 mM in the final PCR vol of 20 µl. Since Mg^{2+} comes from the restriction enzyme buffer, it was not included in the reaction mixture when amplifying secondarily cut cDNA. Bands were extracted from the display gels as described by Liang *et al.* (1995 *Curr. Opin. Immunol.* 7:274-280), reamplified using the 5' and 3' primers, and subcloned into pCR-Script with high efficiency using the

PCR-Script cloning kit from Stratagene. Plasmids were sequenced by cycle sequencing on an ABI automated sequencer.

A comparison of quiescent neutrophils to bacteria-exposed neutrophils identified numerous genes with altered expression levels. Table 8 lists the genes identified by this technology.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure. All patents, patent applications and references referred to in this application are herein incorporated by reference in their entirety.

Table 1. The number of present genes.

Culture	# of genes present
uninduced neutrophils	1182
E. coli	819
yopH	698
KIM5	696
KIM6	1258
3 strains of Y. pestis	526
4 strains of bacteria	428

Table 2. Selected genes that are called absent in neutrophils and called present in bacteria exposed neutrophils.
*EGR1 was called absent in KIM6

Genbank	Seq ID	Gene name	Symbol	Call for neutrophil	Call for E.coli	Call for KIM5	Call for KIM6	Call for yopH	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
L11329	394	Dual specificity phosphatase 2	DUSP2	A	P	P	P	P	78.8	151.4	147.4	44.6
L40377	465	Protease inhibitor 8 (ovalbumin type)	PI8	A	P	P	P	P	3.1	33.4	21.5	17.2
M36820	589	GRO2 oncogene	GRO2	A	P	P	P	P	119.6	114.1	252.0	66.0
M63978	634	Vascular endothelial growth factor	VEGF	A	P	P	P	P	8.0	203.5	298.4	191.3
M80244	654	Solute carrier family 7(cationic amino acid transporter, y+system), member 5	SLC7A5	A	P	P	P	P	39.7	61.6	46.2	30.1
U12767	800	Nuclear receptor subfamily 4, group A, member 3	NR4A3	A	P	P	P	P	4.1	49.9	63.1	45.4
U19261	826	TNF receptor-associated factor 3	TRAF3	A	P	P	P	P	27.4	20.7	8.9	10.8
U64197	964	Small inducible cytokine subfamily A (Cys-Cys), member 20	SCYA20	A	P	P	P	P	72.0	50.3	57.9	13.2
U91616	1047	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NFKBIE	A	P	P	P	P	8.1	69.0	37.7	51.4
X52541	1133	Early growth response 1	EGR1	A	P	A*	P	P	30.5	9.8	12.8	16.4
Z50194	1358	Pleckstrin homology-like domain, family A, member 1	PHLDA1	A	P	P	P	P	27.9	24.0	16.4	8.5

Table 3. Selected genes called absent in neutrophils and E. coli exposed neutrophils and present in Y. pestis exposed neutrophils.

Genbank	Seq ID	Gene name	Symbol	Call for neutrophil	Call for E.coli	Call for KIM5	Call for KIM6	Call for yopH	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
AF001294	37	Tumor suppressing subransferable candidate 3	TSSC3	A	A	P	P	P	2.6	46.2	34.0	13.1
M59040	614	CD44 antigen (homing function and Indian blood group system)	CD44	A	A	P	P	P	4.4	49.3	56.4	33.0
U03106	758	Cyclin-dependent kinase inhibitor 1A(p21, Cip1)	CDKN1A	A	A	P	P	P	5.4	55.5	53.5	30.7

Table 4. Selected genes called absent in neutrophils and called present in E. coli exposed neutrophils.

Genbank	Seq ID	Gene name	Symbol	Call for neutrophil	Call for E.coli	Call for KIM5	Call for KIM6	Call for yopH	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
D90042	312	N-acetyltransferase2 (arylamine N-acetyltransferase)	NAT2	A	P	A	A	A	13.3	7.0	-1.5	1.0
L19871	422	Activating transription factor 3	ATF3	A	P	A	A	A	10.8	1.0	3.3	3.9
M31166	561	Pentaxin-related gene, rapidly induced by IL-1 beta	PTX3	A	P	P	P	A	11.3	10.9	6.1	3.3
U26403	848	Ephrin-A5	EFNA5	A	P	A	A	A	13.3	3.1	1.0	1.1
U92014	1050	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence		A	P	A	P	A	11.7	1.0	2.7	1.0
X03656	1071	Colony stimulating factor 3 (granulocyte)	CSF3	A	P	A	A	A	16.4	-4.0	-4.0	-4.0
X52213	1131	Leukocyte tyrosine kinase	LTK	A	P	A	A	A	11.8	6.4	3.4	6.2
X81372	1257	Biphenylhydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	BPHL	A	P	P	A	A	11.1	13.5	3.0	3.4
X84746	1265	ABO blood group (transferase A. alph 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferse)	ABO	A	P	P	P	A	10.0	7.0	4.1	4.7

Table 5. Selected genes that are called present in neutrophils and are either called absent or present in bacteria exposed neutrophils.

Genbank	Seq ID	Gene name	Symbol	Call for neutrophil	Call for E.coli	Call for KIM5	Call for KIM6	Call for yopH	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
AF000152	34	OS-4 protein		P	A	A	A	A	-25.5	-66.8	-66.8	-66.8
D13640	167	KIAA0015 gene product		P	A	A	A	A	-62.4	-39.7	-9.1	-3.0
D79985	270	DiGeorge syndrome critical region gene 2	DGCR2	P	A	A	A	A	-2.0	-42.1	-42.1	-42.1
S77763	731	Nuclear factor (erythroid-derived 2), 45kD	NFE2	P	A	A	A	A	-3.0	-90.4	-90.4	-22.4

Table 6. Selected genes that are called present in all conditions.

Genbank	Seq ID	Gene name	Symbol	Call for neutrophil	Call for E.coli	Call for KIM5	Call for KIM6	Call for yopH	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
D14874	178	Adrenomedullin	ADM	P	P	P	P	P	2.3	5.5	4.2	2.5
L20941	424	Ferritin, heavy polypeptide 1	FTH1	P	P	P	P	P	3.2	4.0	1.1	3.6
M15395	505	Integrin, beta 2 (antigenCD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	ITGB2	P	P	P	P	P	-5.1	-4.0	-3.5	-4.2
X17042	1118	Proteoglycan 1, secretory granule	PRG1	P	P	P	P	P	1.9	4.4	3.2	1.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
39830_at	AA044823	1	zk72a10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:488346 3' similar to gb:L19527 60S RIBOSOMAL PROTEIN L27 (HUMAN);, mRNA sequence.	-1.3	-1.5	-2.3	-9.0
32564_at	AA083129	2	zn31a06.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:549010 3' similar to gb:L25085 PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT (HUMAN);, mRNA sequence.	-6.5	-9.8	-1.8	-2.4
34319_at	AA131149	3	zo16d05.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587049 5' similar to gb:X65614 S-100P PROTEIN (HUMAN);, mRNA sequence.	1.2	1.9	1.5	1.2
38432_at	AA203213	4	zx57e04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446622 5' similar to gb:M13755 INTERFERON-INDUCED 17 KD PROTEIN (HUMAN);, mRNA sequence.	-2.0	-19.2	-19.2	-19.2
36027_at	AA418779	5	zv98d05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767817 5' similar to SW:RPB6_HUMAN P41584 DNA-DIRECTED RNA POLYMERASE II 14.4 KD POLYPEPTIDE ;, mRNA sequence.	1.2	-1.3	-2.0	-1.6
39581_at	AA570193	6	nf38c11.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:916052 similar to gb:X05978 CYSTATIN A (HUMAN);, mRNA sequence.	-1.1	3.4	-1.5	2.3
39086_g_at	AA768912	7	nz82h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302011 3' similar to gb:M94556 SINGLE-STRANDED DNA-BINDING PROTEIN MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.	1.4	2.0	-1.2	-3.0
38287_at	AA808961	8	nw16h03.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1240661 3' similar to gb:Z14977_rna1 PROTEASOME CHAIN 7 (HUMAN);, mRNA sequence.	-2.3	-1.8	-2.6	-2.5
36347_f_at	AA873858	9	oh79b10.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1473211 3' similar to gb:X57138_rna1 HISTONE H2B.2 (HUMAN);, mRNA sequence.	-1.0	1.2	-1.1	1.0
35607_at	AA934573	10	oo67b04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571215 3' similar to gb:M54911_rna1 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);, mRNA sequence.	2.8	1.0	1.0	1.0
41764_at	AA976838	11	oq35c12.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1588342 3' similar to gb:X00570 APOLIPOPROTEIN C-I PRECURSOR (HUMAN);, mRNA sequence.	2.5	1.2	1.0	1.0
33116_f_at	AA977163	12	oq25a04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587342 3' similar to gb:X53505 40S RIBOSOMAL PROTEIN S12 (HUMAN);, mRNA sequence.	1.2	-1.7	-1.3	-2.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
33117_r_at	AA977163	12	oq25a04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587342 3' similar to gb:X53505 40S RIBOSOMAL PROTEIN S12 (HUMAN);, mRNA sequence.	1.2	-17.0	-1.3	-3.9
41760_at	AA978033	13	oq55e04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1590270 3' similar to gb:X15822 CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (HUMAN);, mRNA sequence.	-1.5	1.5	-1.3	-1.1
378_s_at	AB000381	14	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds.	5.1	1.0	1.0	1.0
32180_s_at	AB000461	16	Homo sapiens mRNA, complete cds, clone:RES4-22C.	1.3	1.9	1.0	-2.8
35777_at	AB000468	17	Homo sapiens mRNA for zinc finger protein, complete cds, clone:RES4-26.	1.8	-13.9	-13.9	-13.9
32801_at	AB002315	18	Human mRNA for KIAA0317 gene, complete cds.	-1.4	2.2	1.2	-6.6
32487_s_at	AB002533	19	Homo sapiens mRNA for Qip1, complete cds.	-2.0	-1.6	-1.8	-1.8
38259_at	AB002559	20	Homo sapiens mRNA for hunc18b2, complete cds.	1.1	-1.4	-2.1	-1.6
32775_r_at	AB006746	21	Homo sapiens hMmTRA1b mRNA, complete cds.	-10.5	1.2	2.4	1.4
766_at	AB006782	22	Homo sapiens mRNA for galectin-9 isoform, complete cds.	-1.5	-36.1	-1.9	-4.4
31936_s_at	AB007890	23	Homo sapiens mRNA for KIAA0430 protein, partial cds.	-44.6	-3.7	-5.0	-5.8
32335_r_at	AB009010	24	Homo sapiens mRNA for polyubiquitin UbC, complete cds.	-1.5	2.7	-6.1	2.8
38735_at	AB011085	25	Homo sapiens mRNA for KIAA0513 protein, complete cds.	-11.0	-2.3	-2.5	-3.5
38809_s_at	AB011091	26	Homo sapiens mRNA for KIAA0519 protein, complete cds.	-13.2	-2.4	-2.8	-2.0
36623_at	AB011406	27	Homo sapiens mRNA for alkalin phosphatase, complete cds.	-1.2	-1.9	-3.1	-2.1
41193_at	AB013382	28	Homo sapiens mRNA for DUSP6, complete cds.	2.5	6.5	2.3	1.0
36231_at	AC002073	30	#N/A	1.0	1.9	1.1	-2.7
31676_at	AC003973	31	Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.	3.4	1.0	1.0	1.0
32901_s_at	AC005192	32	Homo sapiens BAC clone CTB-163K11 from 7q31, complete sequence.	-7.8	-2.4	-2.0	-2.2
32490_at	AC005955	33	Homo sapiens chromosome 19, cosmid R32065, complete sequence.	-3.9	-1.4	-2.4	-1.8
41202_s_at	AF000152	34	Homo sapiens OS-4 protein (OS-4) mRNA, complete cds.	-25.5	-66.8	-66.8	-66.8
37967_at	AF000424	35	Homo sapiens LST1 mRNA, cLST1/C splice variant, complete cds.	-1.1	-1.8	-2.9	-1.9
38110_at	AF000652	36	Homo sapiens syntenin (sycl) mRNA, complete cds.	-1.2	1.6	1.4	-1.1
31888_s_at	AF001294	37	Homo sapiens IPL (IPL) mRNA, complete cds.	2.6	46.2	34.0	13.1
39688_at	AF001433	38	Human requiem (HREQ) mRNA, complete cds.	-1.0	-29.3	1.5	2.0
41819_at	AF001862	40	Homo sapiens FYN binding protein mRNA, complete cds.	1.2	-3.3	-4.6	-14.9
36172_s_at	AF002163	41	Homo sapiens delta-adaptin mRNA, complete cds.	-5.0	-1.7	1.2	1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
35926_s_at	AF004230	42	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7) mRNA, complete cds.	1.1	-1.9	-2.1	-1.8
337_at	AF005043	43	Homo sapiens poly(ADP-ribose) glycohydrolase (hPARG) mRNA, complete cds.	9.7	1.0	1.0	1.0
38270_at	AF005043	43	Homo sapiens poly(ADP-ribose) glycohydrolase (hPARG) mRNA, complete cds.	9.7	1.0	1.0	1.0
39997_at	AF005664	44	Homo sapiens properdin (PFC) gene, complete cds.	-1.5	-2.2	-2.8	-2.5
1867_at	AF005775	45	Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternatively spliced, complete cds.	4.0	2.0	1.3	1.1
1868_g_at	AF005775	45	Homo sapiens caspase-like apoptosis regulatory protein (clarp) mRNA, alternatively spliced, complete cds.	4.0	1.6	1.5	1.1
34691_f_at	AF006087	47	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.	-1.1	1.9	1.5	1.1
34692_r_at	AF006087	47	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.	-1.1	1.2	-1.1	1.5
40045_g_at	AF009425	48	Homo sapiens clone 22 mRNA, alternative splicing variant alpha-2, complete cds.	1.0	19.7	3.0	1.9
37311_at	AF010400	50	Homo sapiens transaldolase-related protein gene, exons 3-8 and complete cds.	-1.8	-2.8	-4.0	-2.9
31408_at	AF012270	51	Homo sapiens visual pigment-like receptor peropsin (Rrh) mRNA, complete cds.	3.2	1.2	4.5	9.7
33689_s_at	AF012434	52	Homo sapiens D-dopachrome tautomerase (DDT) gene, exon 3 and complete cds.	1.2	-3.8	-3.8	2.2
39027_at	AF017115	53	Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds.	1.1	-1.4	-6.9	-2.2
32810_at	AF019369	54	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds.	6.7	2.9	1.7	2.4
38974_at	AF021819	55	Homo sapiens RNA-binding protein regulatory subunit mRNA, complete cds.	-3.5	-4.0	-4.0	-3.6
35094_f_at	AF025527	56	Homo sapiens leucocyte immunoglobulin-like receptor-4 (LIR-4) mRNA, complete cds.	-2.2	-2.4	-2.3	-2.2
35095_r_at	AF025527	56	Homo sapiens leucocyte immunoglobulin-like receptor-4 (LIR-4) mRNA, complete cds.	-2.2	-1.3	-15.6	-1.3
38584_at	AF026939	58	Homo sapiens CIG49 (cig49) mRNA, complete cds.	-5.7	-4.0	-6.4	-10.2
34481_at	AF030227	59	Homo sapiens vav proto-oncogene, exon 27, and complete cds.	-1.4	-1.3	-2.4	-1.3
36417_s_at	AF035295	60	Homo sapiens clone 23623 mRNA, partial cds.	-5.3	-1.3	-1.3	-1.4
32851_at	AF036956	61	Homo sapiens neuroblastoma apoptosis-related RNA binding protein (NAPOR-1) mRNA, complete cds.	-1.1	-18.7	-18.7	-18.7

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
33668_at	AF037643	62	Homo sapiens 60S ribosomal protein L12 (RPL12) pseudogene, partial sequence.	1.2	-16.1	-6.2	-1.6
34281_at	AF039555	63	Homo sapiens visinin-like protein 1 (VSNL1) mRNA, complete cds.	1.0	15.0	-1.1	3.1
39075_at	AF040958	64	Homo sapiens lysosomal neuraminidase precursor, mRNA, complete cds.	2.1	2.1	4.3	3.1
37715_at	AF045184	65	Homo sapiens nuclear receptor coactivator NCoA-62 mRNA, complete cds.	-5.6	-3.5	-2.4	-2.0
37215_at	AF046798	66	Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and complete cds.	-1.1	-46.4	-2.7	-3.6
33422_at	AF052155	67	Homo sapiens clone 24761 mRNA sequence.	-2.1	1.9	-2.3	-1.8
38831_f_at	AF053356	68	#N/A	-1.3	-1.5	-1.6	-1.7
38832_r_at	AF053356	68	#N/A	-1.3	1.1	-2.4	-1.4
39740_g_at	AF054187	69	Homo sapiens alpha NAC mRNA, complete cds.	-3.1	-1.9	-2.0	-4.3
39739_at	AF054187	69	Homo sapiens alpha NAC mRNA, complete cds.	-3.1	-3.3	-1.7	-8.2
38624_at	AF054506	70	Homo sapiens erythroid K:Cl cotransporter splicing isoform 2 (KCC1) mRNA, complete cds.	3.9	9.1	4.1	4.9
39733_at	AF055001	71	Homo sapiens clone 24560 unknown mRNA, complete cds.	-13.1	1.4	1.1	1.5
36570_at	AF068862	73	Homo sapiens BAC clone 157K21 from 8q21, complete sequence.	4.5	1.0	1.0	1.0
37719_at	AF070539	74	Homo sapiens clone 24433 myelodysplasia/myeloid leukemia factor 2 mRNA, complete cds.	-1.1	1.3	1.1	-1.2
36981_at	AF070649	76	Homo sapiens clone 24452 mRNA sequence.	-5.8	-5.8	-4.3	-5.8
40998_at	AF071309	77	Homo sapiens OPA-containing protein mRNA, complete cds.	-1.3	-1.1	-1.2	1.1
38035_at	AF072928	78	Homo sapiens myotubularin related protein 6 mRNA, partial cds.	-2.9	1.1	1.4	-3.6
37233_at	AF079167	79	Homo sapiens lectin-type oxidized LDL receptor (OLR1) gene, exons 4, 5, and 6, and complete cds.	7.4	193.0	100.1	53.0
36378_at	AF085807	80	Homo sapiens uroplakin Ia mRNA, partial cds.	1.0	1.3	-1.4	1.3
32804_at	AF091263	81	Homo sapiens RNA binding motif protein 5 (RBM5) mRNA, complete cds.	-12.4	-21.5	-9.7	-21.5
41153_f_at	AF102803	82	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	-1.5	-4.2	-1.8	-7.4
41096_at	AI126134	83	qd77c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735496 3' similar to gb:A12027_cds1 CALGRANULIN A (HUMAN);, mRNA sequence.	2.8	-1.5	-1.1	-2.3
33372_at	AI189226	84	qd04h11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1722789 3' similar to SW:RB31_HUMAN Q13636 RAS-RELATED PROTEIN RAB-31. [1] ;, mRNA sequence.	-7.8	-1.2	-1.5	-1.7

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
41793_at	AI288757	85	qm11h01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881553 3' similar to SW:SUR_HUMAN Q09428 SULFONYLUREA RECEPTOR. ;, mRNA sequence.	1.8	7.2	1.8	7.2
37389_at	AI346580	86	qp51f08.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926567 3' similar to TR:O00193 O00193 SMALL ACIDIC PROTEIN. ;, mRNA sequence.	-1.1	1.9	1.2	-1.1
39689_at	AI362017	87	qy39a10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014362 3' similar to gb:X52255_rna1 CYSTATIN C PRECURSOR (HUMAN);, mRNA sequence.	-1.4	-1.5	-2.4	-2.6
31776_at	AI446234	88	tj25g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2142594 3' similar to TR:Q07604 Q07604 PRE-T/NK CELL-ASSOCIATED PROTEIN 1F6 ;, mRNA sequence.	-4.5	1.7	-8.3	-3.3
36171_at	AI521453	89	th60h07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122717 3' similar to SW:P15_HUMAN P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 ;, mRNA sequence.	-1.3	2.5	2.9	1.0
39133_at	AI525379	90	PT1.1_06_H01.r tumor1 Homo sapiens cDNA 5', mRNA sequence.	-1.2	-4.4	-1.4	-1.0
41194_at	AI525652	91	PT1.3_04_C04.r tumor1 Homo sapiens cDNA 5', mRNA sequence.	-1.1	-1.4	-1.8	-2.6
38080_at	AI525665	92	PT1.3_04_D06.r tumor1 Homo sapiens cDNA 5', mRNA sequence.	-1.5	1.1	-1.4	-4.3
39345_at	AI525834	93	PT1.3_06_D01.r tumor1 Homo sapiens cDNA 5', mRNA sequence.	-1.0	-1.3	1.2	-1.3
32744_at	AI526078	94	DU3.2-7.G08.r DU-145 Homo sapiens cDNA 5', mRNA sequence.	-1.8	1.2	-1.6	-4.4
39921_at	AI526089	95	DU3.2-7.H07.r DU-145 Homo sapiens cDNA 5', mRNA sequence.	-1.2	-2.4	-2.8	-3.1
41206_r_at	AI540925	96	PEC1.2_15_A02.r ecnorm Homo sapiens cDNA 5', mRNA sequence.	-1.2	-1.5	-1.9	-2.8
34891_at	AI540958	97	PEC1.2_15_H01.r ecnorm Homo sapiens cDNA 5', mRNA sequence.	2.2	1.4	1.4	-3.6
38061_at	AI541256	98	pec1.2-3.F11.r ecnorm Homo sapiens cDNA 5', mRNA sequence.	-1.1	1.2	-1.1	-1.2
35278_at	AI541542	99	libtest16.A02.r bvnorm Homo sapiens cDNA 5', mRNA sequence.	-1.1	1.2	-1.1	-1.3
39081_at	AI547258	100	PN001_AH_H08.r yodnorm Homo sapiens cDNA 5', mRNA sequence.	1.2	9.4	1.5	4.0
34893_at	AI557064	101	PT2.1_13_A12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.	-1.7	-1.3	-2.7	-2.2
32748_at	AI557852	102	P6test.G05.r misc Homo sapiens cDNA 5', mRNA sequence.	2.1	1.6	1.8	-1.2
37782_at	AI636761	103	ts89f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238477 3' similar to gb:J00306_cds1 SOMATOSTATIN I PRECURSOR (HUMAN);, mRNA sequence.	4.5	1.4	2.8	6.4
36992_at	AI653621	104	tz21b11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2289213 3' similar to gb:X77584 THIOREDOXIN (HUMAN);, mRNA sequence.	1.1	-3.3	-2.8	-2.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38055_at	AI683748	105	tw53e07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263428 3' similar to SW:RPBY_MOUSE O08740 DNA-DIRECTED RNA POLYMERASE II 13.3 KD POLYPEPTIDE ;, mRNA sequence.	1.2	-7.0	-6.8	-1.2
33458_r_at	AI688098	106	wc92f08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326119 3' similar to gb:M60750_cds1 HISTONE H2B (HUMAN);, mRNA sequence.	-1.2	-4.4	-2.4	-2.0
34381_at	AI708889	107	as86g01.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335632 3' similar to gb:X16560 CYTOCHROME C OXIDASE POLYPEPTIDE VIIC PRECURSOR (HUMAN);, mRNA sequence.	-1.5	1.4	-1.2	-1.2
39856_at	AI708983	108	at02f03.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353949 3' similar to gb:M15661 60S RIBOSOMAL PROTEIN L44 (HUMAN);, mRNA sequence.	-1.8	-1.5	-1.6	-17.1
38085_at	AI740522	109	wg16b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2365237 3' similar to SW:HP1G_MOUSE P23198 HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA ;, mRNA sequence.	-1.4	-1.3	1.1	-3.0
35339_at	AI743606	110	wg51f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2368647 3' similar to gb:X56741 RAS-RELATED PROTEIN RAB-8 (HUMAN);, mRNA sequence.	-2.1	2.0	1.3	2.3
37099_at	AI806222	111	wf26e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356746 3' similar to gb:X52195 5-LIPOXYGENASE ACTIVATING PROTEIN (HUMAN);, mRNA sequence.	1.9	2.2	2.1	-1.4
33813_at	AI813532	112	wj83a09.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409400 3' similar to gb:M32315 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (HUMAN);contains Alu repetitive element;contains element HGR repetitive element ;, mRNA sequence.	-1.6	3.7	2.4	3.4
32609_at	AI885852	113	wl62d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429487 3' similar to gb:L19779 HISTONE H2A.1 (HUMAN);, mRNA sequence.	1.4	3.1	2.6	2.6
39353_at	AI912041	114	wd84b06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338259 3' similar to SW:CH10_HUMAN Q04984 10 KD HEAT SHOCK PROTEIN, MITOCHONDRIAL ;, mRNA sequence.	1.0	9.7	6.2	-1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
36683_at	AI953789	115	wx69d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2548915 3' similar to gb:X53331 MATRIX GLA-PROTEIN PRECURSOR (HUMAN);, mRNA sequence.	2.2	3.2	1.5	2.1
38582_at	AI961220	116	wt15b04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2507503 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);, mRNA sequence.	1.0	6.7	7.8	7.7
39700_at	AI961929	117	wt39g02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2509874 3' similar to gb:U02570 !!!! ALU CLASS C WARNING ENTRY !!!! (HUMAN);, mRNA sequence.	-3.8	-4.0	-7.7	-10.4
41185_f_at	AI971724	118	wr07a04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480814 3' similar to SW:SM32_HUMAN P55855 UBIQUITIN-LIKE PROTEIN SMT3B ;, mRNA sequence.	-1.4	-1.1	-1.3	-2.3
33227_at	AI984234	119	wz57e04.x1 NCI_CGAP_Lu27 Homo sapiens cDNA clone IMAGE:2562174 3' similar to SW:CRF4_HUMAN Q08334 CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR. ;, mRNA sequence.	-3.8	-2.2	-2.8	-1.4
33228_g_at	AI984234	119	wz57e04.x1 NCI_CGAP_Lu27 Homo sapiens cDNA clone IMAGE:2562174 3' similar to SW:CRF4_HUMAN Q08334 CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR. ;, mRNA sequence.	-3.8	-2.2	-3.8	-3.4
39076_s_at	AI991040	120	wu36b05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522097 3' similar to TR:Q14919 Q14919 NC2 ALPHA SUBUNIT. [1] ;, mRNA sequence.	-1.8	1.2	-2.0	-1.3
35597_at	AJ000480	121	Homo sapiens mRNA for C8FW phosphoprotein.	9.0	64.3	46.0	41.4
36118_at	AJ000882	122	Homo sapiens mRNA for steroid receptor coactivator 1e.	1.2	-2.1	-1.6	-1.8
38046_at	AJ005579	123	Homo sapiens mRNA for Prer protein.	-2.5	-3.9	-4.6	-2.5
38971_r_at	AJ011896	124	Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta).	2.2	9.4	3.3	6.3
38970_s_at	AJ011896	124	Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta).	2.2	7.0	4.0	4.9
32178_r_at	AJ011915	125	Homo sapiens mRNA for synaptosome associated protein of 23 kilodaltons, isoform A.	-1.9	1.2	-1.7	1.0
36131_at	AJ012008	126	#N/A	-1.0	2.0	1.1	1.1
40203_at	AJ012375	127	Homo sapiens mRNA for SUI1 protein translation initiation factor.	2.5	6.9	7.0	2.5
35302_at	AJ132712	128	Homo sapiens mRNA for TAP/NXF1 protein (nxf1 gene).	-2.3	-1.2	-1.2	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
32826_at	AJ133133	129	Homo sapiens mRNA for ecto-ATP diphosphohydrolase, isolate C1800.	-2.1	-1.3	-1.3	1.1
39049_at	AJ243937	130	Homo sapiens mRNA for G18.1a and G18.1b proteins (G18.1a and G18.1b genes, located in the class III region of the major histocompatibility complex).	-1.1	-1.6	-2.1	-1.9
38894_g_at	AL008637	131	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS	-1.0	-3.0	-4.5	-3.1
39062_at	AL008726	132	#N/A	-1.4	-1.6	-1.2	1.4
35576_f_at	AL009179	133	#N/A	-1.0	1.1	-1.5	-1.2
32573_at	AL021546	134	#N/A	-2.5	-3.2	-2.1	-4.1
34782_at	AL021938	135	Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	-2.0	1.2	-1.3	-2.1
32408_s_at	AL022101	136	#N/A	1.6	2.7	3.9	1.8
32319_at	AL022310	137	Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A,	6.4	-1.6	-1.6	4.0
41235_at	AL022312	138	#N/A	1.4	4.4	4.5	2.2
39230_at	AL022318	139	#N/A	-1.6	-16.1	-1.8	-1.7
31722_at	AL022326	140	#N/A	-1.1	-1.1	-1.3	-2.3
37421_f_at	AL022723	141	#N/A	-1.0	1.7	-1.7	1.5
37420_i_at	AL022723	141	#N/A	-1.1	-1.4	-1.4	-1.9
31545_at	AL031228	142	#N/A	-1.4	-1.4	-1.2	-1.8
33301_g_at	AL031282	143	#N/A	-6.2	-1.1	-1.5	-1.2
35083_at	AL031670	144	#N/A	1.9	1.4	-1.6	1.2
39652_at	AL031736	145	Human DNA sequence from clone 738P11 on chromosome 1q24.1-24.3. Contains the SCYC1 gene for small inducible cytokine subfamily C, member 1 (lymphotactin) (Lymphotaxin, LTN), a novel gene for a SCYC1 LIKE protein, two RPL7A (60S Ribosomal Protein L7A) pseu	1.0	7.1	1.0	1.0

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37009_at	AL035079	146	#N/A	1.2	-5.1	-3.7	-4.4
38456_s_at	AL049650	147	#N/A	-1.0	3.2	1.6	1.2
38455_at	AL049650	147	#N/A	-1.0	2.2	1.4	-1.1
40975_s_at	AL050258	148	Novel human mRNA similar to mouse tuftelin-interacting protein 10 mRNA, AF097181.	3.0	1.4	-1.2	2.7
40521_at	AL050259	149	Homo sapiens mRNA; cDNA DKFZp564D0782 (from clone DKFZp564D0782); complete cds.	-1.9	-2.0	-4.9	-3.0
36243_at	AL050262	150	Homo sapiens mRNA; cDNA DKFZp564I0682 (from clone DKFZp564I0682); complete cds.	-60.4	-4.7	-20.8	-36.3
34304_s_at	AL050290	151	Homo sapiens mRNA; cDNA DKFZp586G1923 (from clone DKFZp586G1923).	2.7	8.7	7.1	2.6
32749_s_at	AL050396	152	Homo sapiens mRNA; cDNA DKFZp586K1720 (from clone DKFZp586K1720).	3.1	5.5	4.5	4.2
32033_at	AL096780	153	Novel human gene mapping to chomosome 22p13.33 similar to mouse Choline/Ethanolamine Kinase (O55229).	-1.1	-16.3	-14.9	-16.3
38207_at	AW006742	154	wr28g10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489058 3' similar to TR:Q15810 Q15810 CLONE 137308 ORF1 ;, mRNA sequence.	4.6	6.6	11.4	3.9
41551_at	AW044624	155	wy78c04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554662 3' similar to TR:O15258 O15258 RER1 PROTEIN. ;, mRNA sequence.	-3.2	-3.6	-2.6	-2.8
41552_g_at	AW044624	155	wy78c04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554662 3' similar to TR:O15258 O15258 RER1 PROTEIN. ;, mRNA sequence.	-3.2	-2.2	-3.5	-14.6
1447_at	D00761	156	Human mRNA for proteasome subunit HC5.	-1.9	1.1	-1.6	-2.4
1450_g_at	D00763	157	zq51g09.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645184 3' similar to gb:D00763 PROTEASOME COMPONENT C9 (HUMAN);, mRNA sequence.	-5.5	-1.2	-2.1	-8.2
32046_at	D10495	159	Homo sapiens mRNA for protein kinase C delta-type, complete cds.	2.2	4.1	3.0	2.9
1810_s_at	D10495	159	Homo sapiens mRNA for protein kinase C delta-type, complete cds.	2.2	3.8	2.6	2.6
34951_at	D10923	162	Human mRNA for HM74.	6.8	9.0	14.6	13.7
39994_at	D10925	163	Human mRNA for HM145.	1.6	3.7	4.4	1.8
1506_at	D11086	164	Human mRNA for interleukin 2 receptor gamma chain.	1.2	3.7	2.0	2.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1305_s_at	D12620	165	Homo sapiens mRNA for cytochrome P-450LTBV, complete cds.	-1.3	1.9	1.4	1.5
37077_at	D13243	166	Homo sapiens gene for pyruvate kinase L, exon12 and complete cds.	1.0	4.1	3.9	12.7
37384_at	D13640	167	Human mRNA for KIAA0015 gene, complete cds.	-62.4	-39.7	-9.1	-3.0
41215_s_at	D13891	169	Human mRNA for Id-2H, complete cds.	3.2	1.1	2.1	1.3
777_at	D13988	170	Human rab GDI mRNA, complete cds.	-5.0	1.1	-2.6	-1.9
34819_at	D14043	171	Human mRNA for MGC-24, complete cds.	-3.8	-1.3	-1.7	-2.3
347_s_at	D14530	173	Human homolog of yeast ribosomal protein S28, complete cds.	1.1	-7.1	-1.2	-1.3
37359_at	D14658	174	Human mRNA for KIAA0102 gene, complete cds.	-3.7	-2.2	-1.6	-7.3
34760_at	D14664	175	Human mRNA for KIAA0022 gene, complete cds.	1.4	-3.6	-4.9	-5.7
37320_at	D14694	176	Human mRNA for KIAA0024 gene, complete cds.	1.5	3.4	1.3	-1.0
37325_at	D14697	177	Human mRNA for KIAA1293 gene, complete cds.	-4.4	-4.1	-2.0	-4.1
34777_at	D14874	178	Homo sapiens mRNA for adrenomedullin precursor, complete cds.	2.3	5.5	4.2	2.5
38123_at	D14878	179	Human mRNA for protein D123, complete cds.	-1.2	-1.3	-11.4	-13.6
38413_at	D15057	180	Human mRNA for DAD-1, complete cds.	-7.7	2.2	-1.7	-1.9
35770_at	D16469	181	Human mRNA for ORF, Xq terminal portion.	2.2	-2.8	-1.7	-1.2
39741_at	D16481	182	Homo sapiens mRNA for mitochondrial 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein, complete cds.	-4.9	-1.4	-1.6	1.0
40115_at	D16562	183	Human mRNA for ATP synthase gamma-subunit (L-type), complete cds.	-1.5	-6.3	-1.3	-1.1
35723_at	D16581	184	Human mRNA for 8-oxo-dGTPase, complete cds.	1.5	-3.4	-1.8	-1.4
40735_at	D16626	185	Human mRNA for histidase, complete cds.	-2.5	-19.3	-4.7	-19.3
1873_at	D21089	186	Human mRNA for XP-C repair complementing protein (p125), complete cds.	1.6	-6.0	-19.1	-6.4
1874_at	D21090	187	Human mRNA for XP-C repair complementing protein (p58/HHR23B), complete cds.	1.6	-8.8	-6.1	-8.8
36678_at	D21261	188	Human mRNA for KIAA0120 gene, complete cds.	1.5	-1.0	-1.7	-1.2
38031_at	D21853	189	Human mRNA for KIAA0111 gene, complete cds.	1.4	4.7	4.2	3.7
32675_at	D21878	190	Human mRNA for BST-1, complete cds.	-1.8	1.4	1.1	1.5
33656_at	D23661	191	Human mRNA for ribosomal protein L37, complete cds.	1.1	1.2	1.0	1.3
1695_at	D23662	192	Homo sapiens mRNA for ubiquitin-like protein, complete cds.	-1.2	-15.5	-2.1	-1.0
35689_at	D25215	193	Human mRNA for KIAA0032 gene, complete cds.	2.3	1.6	-2.9	1.2
40864_at	D25274	194	Homo sapiens mRNA, clone:PO2ST9.	-15.7	-2.3	-4.1	-2.5
37543_at	D25304	195	Human mRNA for KIAA0006 gene, partial cds.	-1.7	-1.0	-1.2	-3.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
41333_at	D26069	197	Human mRNA for KIAA0041 gene, partial cds.	1.2	-2.5	-2.1	-1.0
1309_at	D26598	199	Human mRNA for proteasome subunit HsC10-II, complete cds.	-1.0	-1.6	-2.5	-3.8
1310_at	D26599	200	Human mRNA for proteasome subunit HsC7-I, complete cds.	-2.0	-1.2	-1.5	-3.4
33154_at	D26600	201	Human mRNA for proteasome subunit HsN3, complete cds.	-1.2	-1.1	-1.8	-2.4
1311_at	D26600	201	Human mRNA for proteasome subunit HsN3, complete cds.	-1.2	-1.3	-1.4	-1.9
32628_at	D28118	202	Human mRNA for DB1, complete cds.	-7.0	-5.9	-2.9	-1.3
351_f_at	D28423	203	Human mRNA for pre-mRNA splicing factor SRp20, 5'UTR (sequence from the 5'cap to the start codon).	3.1	4.1	11.5	-2.8
39699_at	D28476	204	Human mRNA for KIAA0045 gene, complete cds.	1.0	2.1	-1.0	-2.8
37212_at	D28588	205	Human mRNA for KIAA0048 gene, complete cds.	2.8	6.8	1.7	2.6
941_at	D29012	206	Human mRNA for proteasome subunit Y, complete cds.	-1.0	1.0	-1.7	-1.3
1696_at	D29013	207	Human mRNA for DNA polymerase beta, complete cds.	1.7	-5.7	-2.2	1.3
38149_at	D29642	208	Human mRNA for KIAA0053 gene, complete cds.	-7.8	-4.8	-5.5	-1.8
1418_at	D29675	209	Human inducible nitric oxide synthase gene, promoter and exon 1.	9.9	1.0	1.0	1.0
40960_at	D29805	210	Human mRNA for beta-1,4-galactosyltransferase, complete cds.	2.1	1.7	1.1	1.0
40227_at	D29810	211	Human mRNA for unknown product, partial cds.	2.7	-7.3	-1.3	-7.3
41862_at	D29954	212	Human mRNA for KIAA0056 gene, partial cds.	1.4	4.5	-1.2	3.0
1420_s_at	D30655	213	Homo sapiens mRNA for eukaryotic initiation factor 4AII, complete cds.	1.3	1.2	-1.4	-2.7
33444_at	D30756	214	Human mRNA for KIAA0049 gene, complete cds.	1.9	-1.0	-5.4	-1.6
37411_at	D30758	215	Human mRNA for KIAA0050 gene, complete cds.	1.2	-3.3	-2.6	-2.4
36616_at	D31767	216	Human mRNA for KIAA0058 gene, complete cds.	-1.1	-1.1	-1.6	-2.8
36572_r_at	D31885	217	Human mRNA for KIAA0069 gene, partial cds.	-1.6	3.1	1.2	2.0
37651_at	D31888	218	Human mRNA for KIAA0071 gene, partial cds.	1.0	-1.4	-2.6	-8.5
34336_at	D32053	219	Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds.	2.0	1.2	-1.8	-1.6
36188_at	D32257	221	Human GTF3A mRNA for Xenopus transcription factor IIIA homologue, complete cds.	-1.0	1.0	1.0	2.0
33777_at	D34625	222	Human TBXAS1 gene for thromboxane synthase, exon 13.	1.3	-3.3	-4.6	-5.0
1312_at	D38047	223	Human mRNA for 26S proteasome subunit p31, complete cds.	1.1	-1.5	1.1	1.3
1313_at	D38048	224	Human mRNA for proteasome subunit z, complete cds.	1.1	-1.4	-3.5	-3.7
1858_at	D38122	226	Human mRNA for Fas ligand, complete cds.	9.9	2.2	1.0	1.0
738_at	D38524	227	Human mRNA for 5'-nucleotidase.	-5.4	3.1	-1.5	1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38114_at	D38551	229	Human mRNA for KIAA0078 gene, complete cds.	-2.3	-15.7	-3.1	-15.7
36208_at	D42040	231	Human mRNA for KIAA9001 gene, complete cds.	2.1	1.4	1.5	1.7
32788_at	D42063	232	Human mRNA for RanBP2 (Ran-binding protein 2), complete cds.	-1.8	2.3	3.3	4.7
33326_at	D42087	233	Human mRNA for KIAA0118 gene, partial cds.	2.2	8.7	8.0	5.4
314_at	D42138	234	Homo sapiens mRNA for PIG-B, complete cds.	2.0	1.5	-1.9	-1.2
37718_at	D43636	235	Human mRNA for KIAA0096 gene, partial cds.	-7.0	-26.7	-7.2	-26.7
40417_at	D43950	236	Homo sapiens mRNA for KIAA0098 protein, partial cds.	-4.2	-4.8	-3.7	-4.9
38976_at	D44497	237	Human mRNA for actin binding protein p57, complete cds.	-2.3	-2.6	-3.6	-2.6
944_s_at	D49354	239	Human mRNA for enhancer protein in hsp70 gene, partial cds.	9.3	-3.1	-1.3	1.2
37395_at	D49400	240	Homo sapiens mRNA for vacuolar ATPase, complete cds.	-1.1	1.0	2.1	2.8
1185_at	D49410	241	Human gene for interleukin 3 receptor alpha subunit, exon 12 and partial cds.	-5.4	-8.3	-1.3	2.1
39522_at	D49817	242	Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds.	5.2	21.7	13.0	7.8
1836_at	D50310	243	Human mRNA for cyclin I, complete cds.	1.3	1.1	-1.4	-1.6
38597_f_at	D50402	244	Human mRNA for NRAMP1, complete cds.	1.3	2.4	2.4	3.9
38771_at	D50405	245	Human mRNA for RPD3 protein, complete cds.	-1.2	-2.6	-2.5	-14.1
33683_at	D50525	246	Human mRNA for TI-227H.	-1.3	2.2	1.2	-1.7
41627_at	D50645	247	Homo sapiens mRNA for SDF2, complete cds.	-2.5	2.0	1.0	-2.7
946_at	D50663	248	Human mRNA for TCTEL1 gene, complete cds.	-1.9	-10.8	-3.7	-19.6
1815_g_at	D50683	249	Homo sapiens mRNA for TGF-betaIIR alpha, complete cds.	-22.9	-3.4	-10.1	-29.8
1814_at	D50683	249	Homo sapiens mRNA for TGF-betaIIR alpha, complete cds.	-22.9	-14.8	-14.5	-44.8
1904_at	D50692	250	Homo sapiens mRNA for c-myc binding protein, complete cds.	5.1	4.4	-2.6	-1.8
33498_at	D50495	251	Human mRNA for Reg-related sequence derived peptide-2.	2.7	1.0	1.0	2.3
32445_at	D63390	252	Homo sapiens mRNA for acetylhydrolase IB beta-subunit, complete cds.	1.3	3.5	1.1	1.0
39795_at	D63475	253	Human mRNA for KIAA0109 gene, complete cds.	-3.4	-2.0	-3.7	-1.4
40828_at	D63476	254	Human mRNA for KIAA0142 gene, complete cds.	-2.0	2.5	1.2	-1.5
38089_at	D63478	255	Human mRNA for KIAA0144 gene, complete cds.	2.1	-6.4	2.5	1.4
36741_at	D63482	256	Human mRNA for KIAA0148 gene, complete cds.	-2.4	-25.9	-25.9	-4.3
33281_at	D63485	257	Human mRNA for KIAA0151 gene, complete cds.	3.5	1.7	1.2	1.7
37962_r_at	D63506	258	Homo sapiens mRNA for unc-18homologue, complete cds.	-1.0	-2.3	-2.4	-6.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
35895_at	D63710	259	Human ob gene, exon 3 and complete cds.	4.3	1.0	1.0	1.3
32220_at	D63874	260	Human mRNA for HMG-1, complete cds.	-1.6	1.0	-1.5	-1.5
37959_at	D63876	261	Human mRNA for KIAA0154 gene, partial cds.	-3.0	-14.6	-14.6	-14.6
40281_at	D63878	262	Human mRNA for KIAA0158 gene, complete cds.	-2.2	-1.5	-1.4	-1.8
36207_at	D67029	263	Human SEC14L mRNA, complete cds.	-5.2	-10.2	-5.0	-5.3
40140_at	D76444	264	Homo sapiens hkf-1 mRNA, complete cds.	-3.5	2.5	3.8	2.4
39864_at	D78134	265	Homo sapiens mRNA for CIRP, complete cds.	-4.7	-1.9	-2.6	-2.4
1166_at	D78151	266	Human mRNA for 26S proteasome subunit p97, complete cds.	1.1	1.1	-1.3	1.2
1315_at	D78361	267	Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2.	1.1	-1.1	-1.6	-1.5
1424_s_at	D78577	268	Human DNA for 14-3-3 protein eta chain, exon2 and complete cds.	-1.3	-1.4	-2.5	-1.2
40662_g_at	D78579	269	Homo sapiens mRNA for neuron derived orphan receptor, complete cds.	-3.4	22.3	28.8	10.8
40661_at	D78579	269	Homo sapiens mRNA for neuron derived orphan receptor, complete cds.	-3.4	27.8	38.8	9.1
33889_s_at	D79985	270	Human mRNA for KIAA0163 gene, complete cds.	-2.0	-42.1	-42.1	-42.1
38050_at	D79986	271	Human mRNA for KIAA0164 gene, complete cds.	-2.1	-1.5	-3.5	-2.1
37598_at	D79990	272	Human mRNA for KIAA0168 gene, complete cds.	-3.7	-1.5	-1.4	-1.4
32644_at	D79991	273	Homo sapiens mRNA for KIAA0169 protein, partial cds.	2.3	3.2	3.0	3.0
36942_at	D79996	274	Human mRNA for KIAA0174 gene, complete cds.	-1.7	-1.6	-1.7	-2.5
37031_at	D80005	275	Human mRNA for KIAA0183 gene, partial cds.	-2.0	-10.1	-3.0	-10.1
37734_at	D80006	276	Human mRNA for KIAA0184 gene, partial cds.	-2.4	-1.1	-1.2	-2.3
37683_at	D80012	277	Human mRNA for KIAA0190 gene, partial cds.	-1.2	-2.3	-1.8	-6.6
31672_g_at	D82351	278	Human retropseudogene MSSP-1 DNA, complete cds.	1.1	-15.8	-3.6	-4.6
32674_at	D83032	279	Homo sapiens mRNA for nuclear protein, NP220, complete cds.	-2.4	-3.3	-1.7	-1.4
38879_at	D83664	280	Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds.	1.1	-8.1	1.1	-8.1
37292_at	D83785	281	Human mRNA for KIAA0200 gene, complete cds.	1.6	-2.0	-2.2	-3.8
1621_at	D85423	282	Homo sapiens mRNA for Cdc5, partial cds.	10.1	1.0	1.0	1.0
752_s_at	D85429	283	Homo sapiens gene for heat shock protein 40, complete cds.	1.1	-2.6	-1.5	1.2
32691_s_at	D86096	284	Human DNA for prostaglandin EP3 receptor subtype, complete cds.	-5.0	4.5	1.7	2.6
40034_r_at	D86864	286	Homo sapiens mRNA for acetyl LDL receptor, complete cds.	3.8	1.1	3.2	4.0
34387_at	D86960	287	Human mRNA for KIAA0205 gene, complete cds.	-4.1	1.5	-1.4	-1.2
32704_at	D86964	288	Human mRNA for KIAA0209 gene, partial cds.	-2.3	-5.0	-3.2	-3.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37551_at	D86966	289	Human mRNA for KIAA0211 gene, complete cds.	1.2	-1.6	-1.7	-1.5
31898_at	D86967	290	Human mRNA for KIAA0212 gene, complete cds.	1.4	2.2	1.5	2.1
33748_at	D86976	291	Human mRNA for KIAA0223 gene, partial cds.	-2.6	-5.5	-5.8	-3.7
31802_at	D86979	292	Homo sapiens mRNA for KIAA0226 protein, partial cds.	1.9	-1.2	-6.7	-2.6
40971_at	D86982	293	Human mRNA for KIAA0229 gene, partial cds.	-3.0	1.7	-1.4	-1.1
39327_at	D86983	294	Human mRNA for KIAA0230 gene, partial cds.	-2.6	2.8	1.5	1.8
37748_at	D86985	295	Homo sapiens mRNA for KIAA0232 protein, partial cds.	-3.0	-13.5	-3.0	-2.3
39404_s_at	D86988	296	Human mRNA for KIAA0221 gene, complete cds.	-2.1	-33.4	-10.3	-4.7
38393_at	D87434	298	Human mRNA for KIAA0247 gene, complete cds.	1.3	2.2	2.2	1.3
40447_at	D87436	299	Human mRNA for KIAA0249 gene, complete cds.	-1.5	-1.6	-4.0	-29.3
34835_at	D87442	300	Human mRNA for KIAA0253 gene, partial cds.	-1.4	-41.7	-9.5	-5.1
36154_at	D87452	301	Homo sapiens mRNA for KIAA0263 protein, partial cds.	-27.5	-17.4	-4.0	-6.9
37336_at	D87684	302	Homo sapiens mRNA for KIAA0242 protein, partial cds.	-2.0	-4.0	-1.3	-4.0
31907_at	D87735	303	Homo sapiens mRNA for ribosomal protein L14, complete cds.	-2.3	2.0	-1.3	-6.2
36933_at	D87953	304	Human mRNA for RTP, complete cds.	1.2	2.2	-1.0	1.3
34479_at	D88532	305	Homo sapiens mRNA for p55pik, complete cds.	-2.6	8.0	1.0	3.7
33367_s_at	D88674	306	Homo sapiens mRNA for antizyme inhibitor, complete cds.	5.0	16.5	13.5	9.2
1277_at	D89016	307	Homo sapiens mRNA for Neuroblastoma, complete cds.	5.5	-1.5	-2.2	1.0
39624_at	D89078	310	Homo sapiens mRNA for leukotriene b4 receptor, complete cds.	-37.4	1.1	-1.1	1.1
1817_at	D89667	311	Homo sapiens mRNA for c-myc binding protein, complete cds.	-1.0	-3.5	-1.3	-4.8
38912_at	D90042	312	Human liver arylamine N-acetyltransferase (EC 2.3.1.5) gene.	13.3	7.0	-1.5	1.0
723_s_at	G1322-HT5143		Human nuclear ribonucleoprotein particle (hnRNP) C protein mRNA, complete cds.	1.6	4.1	4.7	1.1
324_f_at	G1515-HT1515		#N/A	-1.3	-1.4	1.3	2.9
954_s_at	G1614-HT1614		Human protein phosphatase-1 catalytic subunit mRNA, complete cds.	-24.9	-16.4	-6.2	-3.3
1173_g_at	G172-HT3924		#N/A	2.7	9.6	2.8	5.6
726_f_at	G1751-HT1768		#N/A	-1.3	11.7	3.4	7.5
327_f_at	G1800-HT1823		#N/A	1.2	1.2	-1.2	-2.7
955_at	G1862-HT1897		#N/A	-1.1	-1.0	-1.1	-9.1
1818_at	G1879-HT1919		#N/A	-4.6	-3.4	-2.5	-1.2
956_at	G1980-HT2023		#N/A	-1.7	2.0	1.3	1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
957_at	G2059-HT2114		#N/A	-1.9	1.2	-1.3	-1.2
329_s_at	G2238-HT2321		H.sapiens mRNA for NuMA protein.	-7.4	1.1	-1.2	-1.3
330_s_at	G2259-HT2348		Human HALPHA44 gene for alpha-tubulin, exons 1-3.	-2.5	-1.8	-2.6	-2.1
1663_at	G2325-HT2421		#N/A	4.0	-3.5	-3.5	-3.5
959_at	G2463-HT2559		#N/A	3.6	1.0	1.0	1.0
333_s_at	G2639-HT2735		H.sapiens MSSP-2 mRNA.	1.1	-2.6	-2.5	-3.1
694_at	G2689-HT2785		#N/A	1.0	10.8	3.4	1.0
1842_at	G2724-HT2820		#N/A	3.1	8.6	8.8	6.2
1180_g_at	G2855-HT2995		ae49g08.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:950270 3' similar to gb:Y00371_rna1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN);, mRNA sequence.	-5.3	3.7	2.5	1.4
1179_at	G2855-HT2995		#N/A	-5.3	3.5	3.3	2.7
312_s_at	G3075-HT3236		Human focal adhesion kinase (FAK) mRNA, complete cds.	5.7	2.3	1.0	1.0
1894_f_at	G3236-HT3413		#N/A	-8.4	4.7	1.9	5.7
1164_at	G3344-HT3521		#N/A	-2.7	-3.6	-2.6	-2.7
1142_at	G3432-HT3618		#N/A	-3.0	8.5	1.7	5.3
292_s_at	G3484-HT3678		Homo sapiens clk1 mRNA, complete cds.	-1.6	-2.8	-1.7	-1.3
1903_at	G3521-HT3715		#N/A	-1.3	1.5	1.4	1.2
1630_s_at	G3730-HT4000		Homo sapiens protein tyrosine kinase (Syk) mRNA, complete cds.	-5.3	-23.7	-3.7	-7.3
938_at	G3936-HT4206		#N/A	-2.5	10.8	2.6	1.0
1937_at	G4036-HT4306		#N/A	1.2	-2.5	2.6	3.4
294_s_at	G4120-HT4392		Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.	-6.2	-1.7	-1.0	-2.2
1286_s_at	IG429-HT429		Human B-cell growth factor (BCGF1) mRNA, complete cds.	5.2	1.0	1.0	1.0
706_at	G4582-HT4987		#N/A	-5.7	-3.2	-1.4	-3.2
1150_at	IG620-HT620		#N/A	1.9	6.2	5.1	3.0
31525_s_at	J00153	313	#N/A	1.6	1.9	-2.1	1.7
37039_at	J00194	314	human hla-dr antigen alpha-chain mrna & ivs fragments.	1.6	2.2	1.8	1.4
306_s_at	J02621	315	Human non-histone chromosomal protein HMG-14 mRNA, complete cds.	-1.4	-1.1	-1.2	-2.1
40379_at	J02625	316	Human cytochrome P-450j mRNA, complete cds.	1.0	6.7	1.0	2.3

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
691_g_at	J02783	317	Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	-7.5	1.3	1.9	1.7
1431_at	J02843	318	Human cytochrome P450IIE1 (ethanol-inducible) gene, complete cds.	3.4	4.3	1.1	-2.2
40867_at	J02902	319	Human protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65) mRNA, complete cds.	-1.1	-1.5	-1.1	-1.1
922_at	J02902	319	Human protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65) mRNA, complete cds.	-1.1	-2.0	1.0	-2.8
37023_at	J02923	320	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds.	1.5	2.7	3.2	1.8
36543_at	J02931	321	Human placental tissue factor (two forms) mRNA, complete cds.	32.5	13.5	9.9	1.0
692_s_at	J02947	322	Human extracellular-superoxide dismutase (SOD3) mRNA, complete cds.	1.0	1.7	1.8	3.3
33803_at	J02973	323	Human thrombomodulin gene, complete cds.	1.7	2.1	-1.1	-1.5
39916_r_at	J02984	324	Human insulinoma rig-analog mRNA encoding DNA-binding protein, complete cds.	-2.1	-1.4	-2.5	-1.2
1408_at	J02986	325	Human transforming protein (hst) gene, complete cds.	8.3	4.7	1.0	1.0
37400_at	J03068	326	Human DNF1552 (lung) mRNA, complete cds.	1.6	6.7	2.0	5.2
36795_at	J03077	327	Human co-beta glucosidase (proactivator) mRNA, complete cds.	-1.3	-1.1	-1.4	1.1
40109_at	J03161	328	Human serum response factor (SRF) mRNA, complete cds.	1.0	3.4	2.3	2.7
1409_at	J03161	328	Human serum response factor (SRF) mRNA, complete cds.	1.0	4.9	3.2	2.6
38081_at	J03459	330	Human leukotriene A-4 hydrolase mRNA, complete cds.	-2.2	-1.4	-2.2	-4.4
41146_at	J03473	331	Human poly(ADP-ribose) synthetase mRNA, complete cds.	1.3	-1.1	-3.2	1.1
40435_at	J03592	332	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8.	-1.5	1.5	-1.6	-1.3
40436_g_at	J03592	332	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8.	-1.5	-4.1	-1.2	1.8
307_at	J03600	333	Human lipoxygenase mRNA, complete cds.	-1.6	-5.8	-4.8	-3.5
310_s_at	J03778	334	Human mRNA for microtubule-associated tau protein.	7.2	1.0	1.0	1.0
39728_at	J03909	336	Human gamma-interferon-inducible protein (IP-30) mRNA, complete cds.	-1.0	3.5	2.8	4.7
925_at	J03909	336	Human gamma-interferon-inducible protein (IP-30) mRNA, complete cds.	-1.0	3.4	3.4	4.2
38533_s_at	J03925	337	Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds.	1.0	-2.4	-2.7	-2.5
1158_s_at	J04046	338	Human calmodulin mRNA, complete cds.	1.6	-9.3	-4.0	-3.6
1519_at	J04102	339	Human erythroblastosis virus oncogene homolog 2 (ets-2) mRNA, complete cds.	16.8	64.5	34.3	17.4
41221_at	J04173	342	Homo sapiens phosphoglycerate mutase (PGAM-B) mRNA, complete cds.	-1.3	-1.8	-4.2	-2.8
39758_f_at	J04182	343	Homo sapiens lysosomal membrane glycoprotein-1 (LAMP1) mRNA, complete cds.	-3.1	1.2	1.5	1.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37670_at	J04543	344	Human synexin mRNA, complete cds.	-2.4	2.1	-1.1	-3.4
1288_s_at	J04617	345	Human elongation factor EF-1-alpha gene, complete cds.	1.5	3.4	3.8	2.2
31697_s_at	J04755	346	Human ferritin H processed pseudogene, complete cds.	3.2	3.4	-1.6	2.9
2093_s_at	J04977	347	Human Ku (p70/p80) subunit mRNA, complete cds.	-5.4	-1.2	-1.8	-2.2
679_at	J04990	348	Human cathepsin G gene, complete cds.	3.4	-2.7	1.6	1.4
1520_s_at	J05008	349	Homo sapiens endothelin-1 (EDN1) gene, complete cds.	76.7	249.6	57.5	30.6
31859_at	J05070	350	Human type IV collagenase mRNA, complete cds.	1.5	1.2	1.1	1.3
1119_at	J05249	351	Human replication protein A 32-kDa subunit mRNA, complete cds.	-1.9	1.7	1.4	1.1
37413_at	J05257	352	Homo sapiens (clones MDP4, MDP7) microsomal dipeptidase (MDP) mRNA, complete cds.	-2.8	6.2	2.1	2.9
40695_at	J05272	353	Human IMP dehydrogenase type 1 mRNA complete cds.	-1.0	-2.4	-4.0	-1.8
36036_at	J05500	354	Human beta-spectrin (SPTB) mRNA, complete cds.	1.8	4.5	1.9	-1.4
40507_at	K03195	355	Human (HepG2) glucose transporter gene mRNA, complete cds.	1.8	1.5	-1.3	2.3
686_s_at	K03498	356	Human endogenous retrovirus HERV-K22 pol and envelope ORF region.	-1.4	-1.7	-1.4	1.4
39122_at	K03515	357	Human neuroleukin mRNA, complete cds.	1.3	3.0	-1.7	1.1
35601_at	L00022	358	Human Ig active heavy chain epsilon-1 gene, constant region.	-1.8	17.2	4.6	19.5
32855_at	L00352	359	Human low density lipoprotein receptor gene, exon 18.	9.4	5.7	8.8	6.3
32469_at	L00693	360	Human carcinoembryonic antigen (CGM1) mRNA, complete cds.	1.0	2.5	1.1	1.8
33619_at	L01124	361	Human ribosomal protein S13 (RPS13) mRNA, complete cds.	1.0	-1.1	-1.8	-4.5
36809_at	L01664	362	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds.	-1.3	2.0	1.3	1.4
31596_f_at	L02326	363	Homo sapiens (clone Hu lambda-17) lambda-like gene, complete cds.	-3.0	2.9	1.6	2.2
688_at	L02426	364	Human 26S protease (S4) regulatory subunit mRNA, complete cds.	-2.8	1.7	-1.7	-1.5
274_at	L04282	365	Human CACCC box-binding protein mRNA, complete cds.	-1.2	-1.7	-8.4	-9.3
669_s_at	L05072	366	Homo sapiens interferon regulatory factor 1 gene, complete cds.	-4.8	-2.4	-2.2	-3.1
31708_at	L05095	367	Homo sapiens ribosomal protein L30 mRNA, complete cds.	-1.1	-2.1	-1.3	-2.5
1125_s_at	L05424	368	Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform.	4.4	19.7	24.3	28.7
36930_at	L05425	369	Homo sapiens nucleolar GTPase mRNA, complete cds.	1.1	1.8	2.0	6.0
670_s_at	L05515	370	Homo sapiens cAMP response element-binding protein (CRE-BP1) mRNA, complete cds.	-3.9	-12.2	-12.2	-12.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
39531_at	L06237	371	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.	5.2	1.0	1.8	1.0
32438_at	L06498	372	Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.	1.2	-1.8	-1.2	-1.7
31962_at	L06499	373	Homo sapiens ribosomal protein L37a (RPL37A) mRNA, complete cds.	1.3	-1.4	-1.9	-2.5
649_s_at	L06797	374	Human (clone L5) orphan G protein-coupled receptor mRNA, complete cds.	1.3	3.4	5.3	4.1
1774_at	L06895	375	Homo sapiens antagonizer of myc transcriptional activity (Mad) mRNA, complete cds.	1.7	1.5	1.6	-1.0
34543_at	L06895	375	Homo sapiens antagonizer of myc transcriptional activity (Mad) mRNA, complete cds.	1.7	1.5	4.0	2.1
650_s_at	L07044	376	Homo sapiens calcium/calmodulin-dependent protein kinase (CAMK) isoform B mRNA sequence.	-1.2	-12.6	-4.4	-2.7
32146_s_at	L07261	377	Human alpha adducin mRNA, partial cds including alternate exons A and B.	-5.0	1.2	-6.3	-2.9
37713_at	L07548	378	Human aminoacylase-1 (ACY1) mRNA, complete cds.	5.8	4.4	4.7	1.3
36600_at	L07633	380	Homo sapiens (clone 1950.2) interferon-gamma IEF SSP 5111 mRNA, complete cds.	1.1	-2.3	-2.5	-1.8
276_at	L08069	381	Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds.	1.5	4.7	3.4	2.3
656_at	L08488	383	Human inositol polyphosphate 1-phosphatase mRNA, complete cds.	-3.0	9.2	4.3	2.4
37697_s_at	L08666	384	Homo sapiens porin (por) mRNA, complete cds and truncated cds.	2.2	1.6	-1.4	-2.0
37309_at	L09159	385	Homo sapiens RHOA proto-oncogene multi-drug-resistance protein mRNA, 3' end.	1.1	1.1	-1.2	-1.2
34890_at	L09235	386	Human vacuolar ATPase (isoform VA68) mRNA, complete cds.	-8.0	-1.5	-2.0	-4.4
33012_at	L09753	387	Homo sapiens CD30 ligand mRNA, complete cds.	7.1	14.9	10.3	9.4
31331_at	L10123	388	Homo sapiens surfactant protein A mRNA, complete cds.	1.3	7.4	1.0	1.0
40125_at	L10284	389	Homo sapiens integral membrane protein, calnexin, (IP90) mRNA, complete cds.	1.2	3.5	2.0	3.2
41469_at	L10343	390	Huma elafin gene, complete cds.	6.1	26.6	9.9	8.3
33123_at	L10379	391	Human (clone CTG-B45d) mRNA sequence.	5.3	12.5	1.8	1.0
1499_at	L10413	392	Human farnesyltransferase alpha-subunit mRNA, complete cds.	-1.1	-1.2	-2.4	-1.4
1131_at	L11285	393	Homosapiens ERK activator kinase (MEK2) mRNA.	1.2	-5.3	-2.9	-2.5
1292_at	L11329	394	Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.	78.8	151.4	147.4	44.6
657_at	L11373	395	Human protocadherin 43 mRNA, complete cds for abbreviated PC43.	-1.9	-9.6	-1.9	-9.6
31546_at	L11566	396	Homo sapiens ribosomal protein L18 (RPL18) mRNA, complete cds.	-8.6	-15.5	-1.4	-1.6
932_i_at	L11672	397	Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.	2.0	2.6	1.5	1.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
934_at	L11702	398	Human phospholipase D mRNA, complete cds.	1.0	5.2	1.4	4.3
935_at	L12168	399	Homo sapiens adenylyl cyclase-associated protein (CAP) mRNA, complete cds.	1.0	-1.2	-1.4	-1.8
31506_s_at	L12691	400	Human neutrophil peptide-3 gene, complete cds.	1.2	-2.3	-1.1	-2.5
38789_at	L12711	401	Homo sapiens transketolase (tk) mRNA, complete cds.	-1.8	-6.5	-6.7	-5.3
40592_at	L13329	402	Homo sapiens iduronate-2-sulfatase (IDS) gene, complete cds.	-2.9	1.8	-1.1	-1.2
32569_at	L13385	403	Homo sapiens(clone 71) Miller-Dieker lissencephaly protein (LIS1) mRNA, complete cds.	-4.5	-3.6	-1.4	-5.3
278_at	L13436	404	Homo sapiens guanylate cyclase mRNA, complete mature peptide.	1.3	6.0	-1.7	3.9
1728_at	L13689	406	Human prot-oncogene (BMI-1) mRNA, complete cds.	4.4	3.8	3.1	2.4
39037_at	L13773	407	Human AF-4 mRNA, complete cds.	-3.3	-13.6	-6.1	-13.6
38129_at	L13943	408	Human glycerol kinase (GK) mRNA exons 1-4, complete cds.	1.1	5.0	4.3	2.8
36672_at	L13977	409	Human prolylcarboxypeptidase mRNA, complete cds.	-2.2	-6.3	-2.2	-1.5
36991_at	L14076	410	Human pre-mRNA splicing factor SRp75 mRNA, complete cds.	-3.6	-20.6	-7.7	-20.6
1907_at	L14812	411	Human retinoblastoma related protein (p107) mRNA, complete cds.	6.1	4.0	1.0	3.7
37497_at	L16499	412	Human orphan homeobox protein (PRH) mRNA, complete cds.	-2.8	1.3	-7.4	-7.4
35434_at	L16794	413	Human transcription factor (MEF2) mRNA, complete cds.	-5.1	3.0	2.1	2.0
38637_at	L16895	414	Human lysyl oxidase (LOX) gene, exon 7.	1.0	10.2	1.8	-1.4
35893_s_at	L17418	415	Human complement receptor type 1 (alleles S and F) gene, exon 47 and complete cds's.	1.3	1.2	-1.9	-8.1
1271_g_at	L19067	416	Human NF-kappa-B transcription factor p65 subunit mRNA, complete cds.	1.2	2.8	1.4	1.4
36645_at	L19067	416	Human NF-kappa-B transcription factor p65 subunit mRNA, complete cds.	1.1	3.6	2.3	3.0
1295_at	L19067	416	Human NF-kappa-B transcription factor p65 subunit mRNA, complete cds.	1.1	2.6	1.7	1.7
1272_at	L19161	417	Human translation initiation factor eIF-2 gamma subunit mRNA, complete cds.	1.5	1.0	3.3	1.0
35934_at	L19161	417	Human translation initiation factor eIF-2 gamma subunit mRNA, complete cds.	1.5	-1.8	2.5	-1.8
33768_at	L19267	418	Homo sapiens 59 protein mRNA, 3' end.	1.3	2.8	3.0	2.2
664_at	L19593	419	Homo sapiens interleukin 8 receptor beta (IL8RB) mRNA, complete cds.	-3.0	-7.2	-6.2	-7.2
36637_at	L19605	420	Homo sapiens 56K autoantigen annexin XI gene mRNA, complete cds.	-1.4	-1.4	-2.3	-1.4
286_at	L19779	421	Homo sapiens histone H2A.2 mRNA, complete cds.	1.4	4.2	2.6	2.3
287_at	L19871	422	Human activating transcription factor 3 (ATF3) mRNA, complete cds.	10.8	1.0	3.3	3.9
1138_at	L20859	423	Human leukemia virus receptor 1 (GLVR1) mRNA, complete cds.	-5.1	5.1	6.4	5.7

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
33705_at	L20971	425	Human phosphodiesterase mRNA, complete cds.	-1.1	6.3	4.8	2.3
1274_s_at	L22005	426	af17d01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031905 3' similar to SW:UBC3_HUMAN P49427 UBIQUITIN-CONJUGATING ENZYME E2-CDC34 COMPLEMENTING ;contains element TAR1 repetitive element ;, mRNA sequence.	1.1	-6.8	-4.4	-3.5
33635_at	L22075	427	Human guanine nucleotide regulatory protein (G13) mRNA, complete cds.	1.2	-1.3	1.7	1.5
35718_at	L22342	428	Human nuclear phosphoprotein mRNA, complete cds.	-3.0	-21.0	-3.5	-4.4
32372_at	L22569	429	Homo sapiens cathepsin B mRNA, 3' UTR with a stem-loop structure providing mRNA stability.	-7.5	-2.7	-1.1	-1.4
2069_s_at	L23805	430	Human alpha1(E)-catenin mRNA, complete cds.	-1.5	1.2	-2.6	-2.3
36446_s_at	L24521	431	Human transformation-related protein mRNA, 3' end.	-4.7	-4.9	-1.3	-1.4
1394_at	L25080	432	Homo sapiens GTP-binding protein (rhoA) mRNA, complete cds.	1.1	1.3	-1.2	-1.2
38427_at	L25286	433	Homo sapiens alpha-1 type XV collagen mRNA, complete cds.	7.1	1.0	1.9	1.0
32432_f_at	L25899	434	Human ribosomal protein L10 mRNA, complete cds.	-1.0	1.7	1.2	-1.1
288_s_at	L25931	435	Human lamin B receptor (LBR) mRNA, complete cds.	-7.8	-9.2	-5.2	-6.8
34006_s_at	L26318	436	Human protein kinase (JNK1) mRNA, complete cds.	3.8	8.1	3.4	7.2
2071_s_at	L26318	436	Human JNK1 beta2 protein kinase (JNK1B2) mRNA, complete cds.	3.8	10.8	3.3	-1.2
2070_i_at	L26318	436	Human protein kinase (JNK1) mRNA, complete cds.	3.8	1.0	1.0	1.0
36925_at	L26336	437	Human heat shock protein HSPA2 gene, complete cds.	2.8	3.1	1.1	1.1
645_at	L26336	437	Human heat shock protein HSPA2 gene, complete cds.	2.8	1.0	1.0	1.0
36670_at	L26339	438	Human autoantigen mRNA, complete cds.	1.0	-1.6	-3.2	-1.2
36682_at	L27841	439	Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds.	-2.6	4.3	-2.4	1.9
1117_at	L27943	440	Homo sapiens cytidine deaminase (CDA) mRNA, complete cds.	-1.4	-1.4	-2.9	-2.0
1118_at	L28175	441	Homo sapiens prostaglandin E2 receptor EP2 subtype mRNA, complete cds.	16.0	13.7	21.0	14.3
38188_s_at	L28821	442	Homo sapiens alpha mannosidase II isozyme mRNA, complete cds.	-8.3	-1.9	-1.9	-1.3
36885_at	L28824	443	Homo sapiens protein tyrosine kinase (Syk) mRNA, complete cds.	-5.3	-15.9	-15.9	-15.9
289_at	L29277	444	Homo sapiens DNA-binding protein (APRF) mRNA, complete cds.	1.3	2.5	2.5	1.7
1398_g_at	L32976	445	Human protein kinase (MLK-3) mRNA, complete cds.	2.4	2.2	1.0	1.4
1397_at	L32976	445	Human protein kinase (MLK-3) mRNA, complete cds.	2.4	2.3	1.6	1.7
1825_at	L33075	446	Homo sapiens ras GTPase-activating-like protein (IQGAP1) mRNA, complete cds.	-1.1	-1.8	-2.0	-1.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1483_at	L34059	447	Homo sapiens cadherin-4 mRNA, complete cds.	3.2	2.0	-1.6	3.0
1399_at	L34587	448	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds.	1.4	-1.0	1.4	-1.0
268_at	L34657	449	Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exon 16 and complete cds.	-1.6	-1.4	-2.4	-4.4
39530_at	L35240	450	Human enigma gene, complete cds.	-1.1	1.1	-1.4	1.0
40568_at	L35249	451	Homo sapiens vacuolar H+-ATPase Mr 56,000 subunit (HO57) mRNA, complete cds.	-4.8	2.0	2.5	1.9
37733_at	L35263	452	Human CSaids binding protein (CSBP1) mRNA, complete cds.	-1.7	-4.9	-22.2	-11.8
40783_s_at	L36151	453	Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.	-1.1	-1.2	1.1	1.3
2075_s_at	L36719	454	Homo sapiens MAP kinase kinase 3 (MKK3) mRNA, complete cds.	3.0	11.1	5.2	6.4
32622_at	L36983	455	Homo sapiens dynamin (DNM) mRNA, complete cds.	1.1	-36.1	-36.1	-2.9
40850_at	L37033	456	Human FK-506 binding protein homologue (FKBP38) mRNA, complete cds.	2.0	-2.4	-1.5	-1.8
1486_at	L37127	457	Homo sapiens RNA polymerase II mRNA, complete cds.	1.2	-26.4	-26.4	-26.4
36186_at	L37368	458	Human (clone E5.1) RNA-binding protein mRNA, complete cds.	1.1	1.3	-1.4	-2.0
37985_at	L37747	459	Homo sapiens lamin B1 gene, exon 11, complete cds.	-7.9	1.4	1.1	-2.1
1487_at	L38487	460	Human estrogen receptor-related protein (hERRa1) mRNA, 3' end, partial cds.	-10.0	3.5	2.3	3.0
36125_s_at	L38696	461	Homo sapiens autoantigen p542 mRNA, complete cds.	1.3	-18.8	-2.9	-2.8
39064_at	L38928	462	Homo sapiens 5,10-methenyltetrahydrofolate synthetase mRNA, complete cds.	-1.6	-1.6	-1.8	-1.1
33657_at	L38941	463	Homo sapiens ribosomal protein L34 (RPL34) mRNA, complete cds.	1.4	-7.6	-1.3	-14.1
632_at	L40027	464	Homo sapiens glycogen synthase kinase 3 mRNA, complete cds.	-1.9	1.3	-1.4	-1.2
36312_at	L40377	465	Homo sapiens cytoplasmic antiproteinase 2 (CAP2) mRNA, complete cds.	3.1	33.4	21.5	17.2
36625_at	L40401	467	Homo sapiens (clone zap128) mRNA, 3' end of cds.	9.2	25.5	7.1	18.0
38216_at	L40411	468	Homo sapiens thyroid receptor interactor (TRIP8) mRNA, 3' end of cds.	2.7	3.9	3.4	3.4
40815_g_at	L40586	469	Homo sapiens iduronate-2-sulphatase (IDS) mRNA, complete cds.	-1.4	1.4	-1.4	-1.2
40814_at	L40586	469	Homo sapiens iduronate-2-sulphatase (IDS) mRNA, complete cds.	-1.4	-4.1	-1.2	-1.4
40887_g_at	L41498	470	Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	1.5	3.3	4.2	2.7
40886_at	L41498	470	Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	1.5	2.4	3.1	1.7
903_at	L42373	471	Homo sapiens phosphatase 2A B56-alpha (PP2A) mRNA, complete cds.	-2.8	-19.1	-4.7	-4.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38844_at	L42451	472	Homo sapiens pyruvate dehydrogenase kinase isoenzyme 2 (PDK2) mRNA, complete cds.	1.1	-1.9	-1.8	3.1
36628_at	L42542	473	Human RLIP76 protein mRNA, complete cds.	-1.0	-17.5	-6.0	-16.1
38376_at	L46590	475	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds.	1.4	-8.4	-1.8	-1.9
37579_at	L47738	476	Homo sapiens inducible protein mRNA, complete cds.	-5.4	-7.1	-2.2	-2.2
32052_at	L48215	477	Homo sapiens beta-globin (HBB) gene, with a to c allele 28 bp 5' to exon 1, (J00179 bases 61971-63802).	1.6	2.8	-2.6	1.8
41203_at	L49380	479	Homo sapiens clone B4 transcription factor ZFM1 mRNA, complete cds.	-1.1	2.6	1.9	2.2
905_at	L76200	481	Human guanylate kinase (GUK1) mRNA, complete cds.	-1.0	2.0	1.1	1.4
34995_at	L76380	482	Homo sapiens (clone HSNME29) CGRP type 1 receptor mRNA, complete cds.	1.7	1.0	1.0	10.1
641_at	L76517	483	Homo sapiens (clone cc44) senilin 1 (PS1; S182) mRNA, complete cds.	-1.2	3.5	3.5	1.9
41792_at	L78207	484	Homo sapiens sulfonylurea receptor (SUR1) mRNA, complete cds.	1.8	2.7	3.2	5.6
36690_at	M10901	485	Human mRNA for alpha-glucocorticoid receptor (clone OB7).	-5.7	-6.5	-4.8	-6.5
39328_at	M11058	486	Human 3-hydroxy-3-methylglutaryl coenzyme A reductase mRNA, complete cds.	1.8	1.6	-1.6	-7.4
1104_s_at	M11717	488	Human MHC class III HSP70-2 gene (HLA), complete cds.	4.4	-1.7	-3.7	-3.3
33218_at	M11730	489	Human tyrosine kinase-type receptor (HER2) mRNA, complete cds.	2.0	1.0	1.0	1.0
1826_at	M12174	490	Human ras-related rho mRNA (clone 6), partial cds.	-2.3	-22.0	-33.7	-8.1
36636_at	M12267	491	Human ornithine aminotransferase mRNA, complete cds.	-9.1	-6.2	1.2	1.1
34638_r_at	M12963	492	Human class I alcohol dehydrogenase (ADH1) alpha subunit mRNA, complete cds.	-1.5	3.2	-3.5	-3.5
31634_at	M13057	493	Human acidic proline-rich protein (PRH1) gene, complete cds.	1.0	2.6	1.5	4.2
35591_at	M13142	494	Human factor XI (blood coagulation factor) mRNA, complete cds.	2.7	-1.6	1.5	-1.2
37377_i_at	M13452	495	Human lamin A mRNA, 3'end.	1.2	-1.1	-2.1	-1.2
37378_r_at	M13452	495	Human lamin A mRNA, 3'end.	1.2	1.0	7.6	1.0
35016_at	M13560	496	Human Ia-associated invariant gamma-chain gene, exon 8, clones lambda-y(1,2,3).	1.2	1.3	-1.5	-1.1
1107_s_at	M13755	497	Human interferon-induced 17-kDa/15-kDa protein mRNA, complete cds.	-2.0	3.0	1.3	1.5
34593_g_at	M13932	498	Human ribosomal protein S17 mRNA, complete cds.	-1.6	-1.3	-1.3	-5.2
34592_at	M13932	498	Human ribosomal protein S17 mRNA, complete cds.	-1.6	-13.0	-1.3	-6.4
32412_at	M13934	499	Human ribosomal protein S14 gene, complete cds.	-1.4	-2.5	-2.6	-1.5
256_s_at	M14199	500	Human laminin receptor (2H5 epitope) mRNA, 5' end.	1.2	-2.2	-1.9	-2.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38590_r_at	M14630	501	Human prothymosin alpha mRNA, complete cds.	1.5	1.2	-1.1	-1.1
38589_i_at	M14630	501	Human prothymosin alpha mRNA, complete cds.	1.5	-2.4	1.2	1.0
908_at	M14660	502	Human ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2.	-13.2	-6.4	-6.2	-21.1
909_g_at	M14660	502	Human ISG-54K gene (interferon stimulated gene) encoding a 54 kDA protein, exon 2.	-13.2	-15.6	-7.6	-15.6
33308_at	M15182	503	Human beta-glucuronidase mRNA, complete cds.	1.7	1.1	-1.2	-2.0
39402_at	M15330	504	Human interleukin 1-beta (IL1B) mRNA, complete cds.	76.7	163.1	41.3	24.4
1402_at	M16038	506	Human lyn mRNA encoding a tyrosine kinase.	-2.0	1.1	1.1	-1.1
32616_at	M16038	506	Human lyn mRNA encoding a tyrosine kinase.	-2.0	1.0	1.2	1.1
37105_at	M16117	507	Human cathepsin G mRNA, complete cds.	3.4	1.9	-2.6	-1.8
33666_at	M16342	508	Human nuclear ribonucleoprotein particle (hnRNP) C protein mRNA, complete cds.	1.4	3.2	3.0	2.2
38034_at	M16505	509	Human steroid sulfatase (STS) mRNA, complete cds.	1.0	4.9	1.4	7.6
40742_at	M16591	510	Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone lambda-a2/1a.	-1.3	-1.4	-2.0	-1.8
2045_s_at	M16592	511	Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone HK24.	-1.3	-1.4	-1.7	-1.7
1779_s_at	M16750	512	Human pim-1 oncogene mRNA, complete cds.	-1.9	-1.1	-3.0	-1.1
41694_at	M17754	515	Human BN51 mRNA, complete cds.	16.2	4.6	-1.6	3.3
31956_f_at	M17886	516	Human acidic ribosomal phosphoprotein P1 mRNA, complete cds.	1.5	-1.6	-1.5	-1.9
31957_r_at	M17886	516	Human acidic ribosomal phosphoprotein P1 mRNA, complete cds.	1.5	-1.6	-2.5	1.2
38587_at	M18079	517	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.	4.8	1.0	1.0	1.0
38356_at	M19481	518	Human follistatin gene, exon 6.	2.7	2.0	-1.2	1.5
1780_at	M19722	519	Human fgr proto-oncogene encoded p55-c-fgr protein, complete cds.	1.5	2.4	2.1	2.5
39443_s_at	M19961	520	Human cytochrome c oxidase subunit Vb (coxVb) mRNA, complete cds.	-1.2	-1.7	-2.0	-1.2
32523_at	M20470	521	Human lymphocyte clathrin light-chain B mRNA, complete cds.	-4.0	-1.4	1.0	-1.2
38657_s_at	M20471	522	Human brain-type clathrin light-chain a mRNA, complete cds.	-1.4	-1.4	-2.0	-1.1
31792_at	M20560	523	Human lipocortin-III mRNA, complete cds.	-1.2	-2.0	-3.5	-5.4
36979_at	M20681	524	Human glucose transporter-like protein-III (GLUT3), complete cds.	1.0	-1.3	-1.7	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
263_g_at	M21154	525	zw47c11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773204 3' similar to gb:M21154 S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (HUMAN);, mRNA sequence.	-5.2	-3.2	-4.5	-22.3
262_at	M21154	525	Human S-adenosylmethionine decarboxylase mRNA, complete cds.	-5.2	-6.3	-5.8	-6.2
1110_at	M21624	527	Human T-cell receptor delta chain mRNA (VJC-region), complete cds.	3.4	3.7	-1.3	2.6
34793_s_at	M22299	528	Human T-plastin polypeptide mRNA, complete cds, clone p4.	3.0	3.2	-1.3	-1.3
39407_at	M22488	530	Human bone morphogenetic protein 1 (BMP-1) mRNA.	4.8	1.0	2.7	11.2
39971_at	M22637	531	Human LYL-1 protein mRNA, complete cds.	-4.5	1.4	-2.0	-1.3
36666_at	M22806	532	Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	-7.5	1.2	1.8	2.2
33994_g_at	M22919	533	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	1.2	1.4	1.1	-1.7
1848_at	M22995	534	Human ras-related protein (Krev-1) mRNA, complete cds.	-1.1	-1.9	-1.9	-4.5
34636_at	M23892	535	Human 15-lipoxygenase mRNA, complete cds.	1.4	-9.2	-2.8	-13.7
34608_at	M24194	536	Human MHC protein homologous to chicken B complex protein mRNA, complete cds.	1.4	-1.7	-2.2	-4.0
34609_g_at	M24194	536	Human MHC protein homologous to chicken B complex protein mRNA, complete cds.	1.4	2.3	1.2	1.1
32640_at	M24283	537	Human major group rhinovirus receptor (HRV) mRNA, complete cds.	7.3	31.6	42.2	15.0
32814_at	M24594	538	Human mRNA for 56-KDa protein induced by interferon.	-3.9	1.0	-1.5	-4.7
915_at	M24594	538	Human mRNA for 56-KDa protein induced by interferon.	-3.9	-1.7	-11.9	-19.5
35294_at	M25077	539	Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.	1.4	-2.9	-2.2	-2.9
31687_f_at	M25079	540	Human sickle cell beta-globin mRNA, complete cds.	2.3	2.5	-2.4	1.7
32378_at	M26252	542	Human TCB gene encoding cytosolic thyroid hormone-binding protein, complete cds.	2.0	-1.2	1.6	1.9
2048_s_at	M26747	543	Human c-erbA mRNA, complete cds.	3.2	11.4	2.5	10.0
1367_f_at	M26880	544	Human ubiquitin mRNA, complete cds.	-1.5	2.4	1.2	2.3
1366_i_at	M26880	544	Human ubiquitin mRNA, complete cds.	-1.5	2.3	2.1	1.8
1368_at	M27492	545	Human interleukin 1 receptor mRNA, complete cds.	2.0	7.1	5.5	2.2
877_at	M27691	546	Human transactivator protein (CREB) mRNA, complete cds.	2.9	-2.6	-1.8	-2.6
1369_s_at	M28130	547	Human beta-thromboglobulin-like protein mRNA, complete cds.	3.6	19.4	1.5	17.5
1116_at	M28170	548	Human cell surface protein CD19 (CD19) gene, complete cds.	-6.0	-1.1	-4.0	1.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1074_at	M28209	549	Homo sapiens GTP-binding protein (RAB1) mRNA, complete cds.	1.8	5.1	7.0	4.4
623_s_at	M28213	550	Homo sapiens GTP-binding protein (RAB2) mRNA, complete cds.	-3.5	-5.2	-1.2	-3.8
36668_at	M28713	551	Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon 9.	1.3	1.7	-1.2	1.1
1076_at	M28983	552	Homo sapiens interleukin 1 alpha (IL 1) mRNA, complete cds.	-1.9	-5.1	-5.1	-5.1
2049_s_at	M29039	553	Human transcription factor junB (junB) gene, 5' region and complete cds.	3.4	2.4	2.0	-1.2
36654_s_at	M29065	554	Human hnRNP A2 protein mRNA.	3.7	2.1	2.3	-1.1
39780_at	M29551	555	Human calcineurin A2 mRNA, complete cds.	1.0	1.0	1.0	10.5
32893_s_at	M30474	557	Human kidney gamma-glutamyl transpeptidase type II mRNA, 3' end.	1.6	19.1	31.0	26.9
879_at	M30818	558	Human interferon-induced cellular resistance mediator protein (MxB) mRNA, complete cds.	-1.6	1.7	1.3	1.4
38733_at	M30938	559	Human Ku (p70/p80) subunit mRNA, complete cds.	-5.4	-3.1	-3.1	-3.0
585_at	M30938	559	Human Ku (p70/p80) subunit mRNA, complete cds.	-5.4	-5.2	-3.4	-5.8
1491_at	M31166	561	Human tumor necrosis factor-inducible (TSG-14) mRNA, complete cds.	11.3	10.9	6.1	3.3
39695_at	M31516	562	Human decay-accelerating factor mRNA, complete cds.	2.1	9.7	8.3	3.5
32315_at	M31520	563	Human ribosomal protein S24 mRNA.	-1.0	1.3	-1.4	-2.1
40137_at	M31724	564	Human phosphotyrosyl-protein phosphatase (PTP-1B) mRNA, complete cds.	1.5	-5.7	-2.0	-5.7
37688_f_at	M31932	565	Human IgG low affinity Fc fragment receptor (FcRIIa) mRNA, complete cds.	-2.4	-3.9	-1.7	-2.7
1375_s_at	M32304	567	Human tissue inhibitor of metalloproteinases-2 (TIMP-2) gene, exon 5 and complete cds.	-1.3	-2.9	-1.5	-1.3
1583_at	M32315	568	Human tumor necrosis factor receptor mRNA, complete cds.	-1.6	3.9	3.2	4.0
36601_at	M33308	570	Human vinculin mRNA, complete cds.	-2.5	1.3	1.3	-1.1
1492_f_at	M33317	571	Human cytochrome P450IIA4 (CYP2A4) mRNA, complete cds.	-2.8	10.4	2.7	4.2
227_g_at	M33336	572	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds.	-2.7	-1.4	-2.0	-2.6
226_at	M33336	572	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds.	-2.7	-1.1	-1.4	-1.7
33913_at	M33509	573	Human HLA-B-associated transcript 2 (BAT2) mRNA, complete cds.	1.1	-2.2	-1.9	-1.1
33838_at	M33519	574	Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds.	1.1	1.2	1.8	-2.2
1081_at	M33764	576	Human ornithine decarboxylase gene, complete cds.	1.9	5.9	2.8	1.3
37014_at	M33882	577	Human p78 protein mRNA, complete cds.	-1.4	-1.5	-2.3	-2.3

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
36215_at	M34181	578	Human testis-specific cAMP-dependent protein kinase catalytic subunit (C-beta isoform) mRNA, complete cds.	7.1	-2.0	-2.0	-2.0
37742_at	M34423	579	Human beta-galactosidase (GLB1) mRNA, complete cds.	-1.8	2.7	-2.6	-2.0
36804_at	M34455	580	Human interferon-gamma-inducible indoleamine 2,3-dioxygenase (IDO) mRNA, complete cds.	-1.1	-2.0	-2.3	-6.9
880_at	M34539	581	Human FK506-binding protein (FKBP) mRNA, complete cds.	-1.4	-1.3	-2.6	-7.6
37907_at	M34677	582	Human nested gene protein gene, complete cds.	-5.9	1.1	-1.5	-2.1
228_at	M35416	583	Human GTP-binding protein (RALB) mRNA, complete cds.	-1.4	-2.7	-1.8	-1.6
39736_at	M35543	584	Human GTP-binding protein (G25K) mRNA, complete cds.	3.6	1.0	1.0	1.0
32806_at	M36035	585	Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds.	-1.3	-2.2	-3.6	-2.0
33987_at	M36340	586	Human ADP-ribosylation factor 1 (ARF1) mRNA, complete cds.	1.4	1.7	1.4	1.8
36585_at	M36341	587	Human ADP-ribosylation factor 4 (ARF4) mRNA, complete cds.	1.7	6.3	6.2	3.9
37418_at	M36653	588	Human Oct-2 factor mRNA, complete cds.	1.0	1.6	1.9	2.9
34022_at	M36821	590	Human cytokine (GRO-gamma) mRNA, complete cds.	8.0	7.0	5.2	7.0
1085_s_at	M37238	592	Human phospholipase C mRNA, complete cds.	-1.3	1.0	-1.2	-1.7
39337_at	M37583	593	Human histone (H2A.Z) mRNA, complete cds.	-1.9	-3.0	-3.4	-17.1
1830_s_at	M38449	594	Human transforming growth factor-beta mRNA, complete cds, clone pTGF-beta-trp114.	1.1	-1.8	-2.3	-1.2
39389_at	M38690	595	Human CD9 antigen mRNA, complete cds.	-2.4	-4.0	-1.2	-2.8
883_s_at	M54915	596	Homo sapiens protein kinase-related oncogene (PIM1) mRNA, complete cds.	-3.0	-1.8	-2.3	-1.2
40159_r_at	M55067	597	Human 47-kD autosomal chronic granulomatous disease protein mRNA, complete cds.	-1.5	-2.4	-5.4	-3.1
40258_at	M55265	598	Human casein kinase II alpha subunit mRNA, complete cds.	1.4	2.0	-1.8	2.8
36313_at	M55267	599	Human EV12 protein gene, exon 1.	-2.6	-1.0	-1.8	-1.6
1267_at	M55284	600	Human protein kinase C-L (PRKCL) mRNA, complete cds.	-1.8	8.9	9.9	-1.2
35735_at	M55542	601	Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.	2.8	7.2	4.6	2.8
32700_at	M55543	602	Human guanylate binding protein isoform II (GBP-2) mRNA, complete cds.	1.8	1.7	1.4	-1.1
39778_at	M55621	603	Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds.	-2.4	1.9	1.5	2.0
31680_at	M55630	604	Human topoisomerase I pseudogene 2.	-1.8	2.8	2.6	2.8
2035_s_at	M55914	605	Human alpha enolase mRNA, complete cds.	-2.2	1.1	-1.4	1.3

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37346_at	M57567	606	Human ADP-ribosylation factor (hARF5) mRNA, complete cds.	1.4	-1.3	-1.8	-1.8
40358_at	M57609	607	Human DNA-binding protein (GLI3) mRNA, complete cds.	3.1	1.0	1.0	1.0
37984_s_at	M57763	608	Human ADP-ribosylation factor (hARF6) mRNA, complete cds.	-2.2	-2.5	-2.0	-1.5
1268_at	M58028	609	Human ubiquitin-activating enzyme E1 (UBE1) mRNA, complete cds.	1.8	-1.3	-2.0	-1.8
1563_s_at	M58286	610	Human tumor necrosis factor receptor mRNA, complete cds.	-1.4	-1.0	-2.2	-3.0
34643_at	M58458	611	Human ribosomal protein S4 (RPS4X) isoform mRNA, complete cds.	1.2	2.9	1.0	1.1
32667_at	M58526	612	Human alpha-5 collagen type IV (COL4A5) mRNA, 3' end.	2.1	1.0	1.0	5.2
38438_at	M58603	613	Human nuclear factor kappa-B DNA binding subunit (NF-kappa-B) mRNA, complete cds.	4.4	15.5	12.2	9.9
1378_g_at	M58603	613	zn44d12.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:550295 3' similar to gb:M58603 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (HUMAN);, mRNA sequence.	4.4	35.5	24.9	22.5
1377_at	M58603	613	Human nuclear factor kappa-B DNA binding subunit (NF-kappa-B) mRNA, complete cds.	4.4	20.6	18.2	10.4
32833_at	M59287	615	Human protein kinase mRNA.	-1.6	-1.1	-1.5	-1.8
34223_at	M59818	616	Human granulocyte colony-stimulating factor receptor (G-CSFR-1) mRNA, complete cds.	1.1	-1.4	-1.6	-1.6
596_s_at	M59820	617	Human granulocyte colony-stimulating factor receptor (G-CSFR-1) mRNA, complete cds.	1.1	-1.2	-1.6	-1.2
237_s_at	M60483	618	Human mRNA for protein phosphatase 2A (alpha-type).	1.1	1.6	1.4	-3.7
32181_at	M60922	620	Human surface antigen mRNA, complete cds.	-1.6	-5.6	-18.4	-6.0
38278_at	M62324	621	Human modulator recognition factor I (MRF-1) mRNA, 3' end.	-8.6	-1.1	-1.8	-1.1
37126_at	M62800	623	Human 52-kD SS-A/Ro autoantigen mRNA, complete cds.	-9.7	-2.9	-3.0	-3.5
239_at	M63138	625	Human cathepsin D (catD) gene, exons 7, 8, and 9.	-1.2	2.0	1.6	2.2
1564_at	M63167	626	Human rac protein kinase alpha mRNA, complete cds.	1.4	-41.7	-5.7	-4.0
38068_at	M63175	627	Human autocrine motility factor receptor mRNA.	6.3	3.3	-1.1	-1.2
35823_at	M63573	628	Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds.	1.0	-17.8	-17.8	-17.8
37220_at	M63835	629	Human IgG Fc receptor I gene, exon 6 and complete cds.	-7.8	-8.6	-2.1	-1.5
1456_s_at	M63838	630	Human interferon-gamma induced protein (IFI 16) gene, complete cds.	-1.0	-4.0	-1.4	-1.4
35380_at	M63896	631	Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.	5.6	1.4	1.0	1.0

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
40365_at	M63904	632	Human G-alpha 16 protein mRNA, complete cds.	2.5	11.8	10.2	9.1
36194_at	M63959	633	Human alpha-2-macroglobulin receptor-associated protein mRNA, complete cds.	-1.7	-32.2	-4.0	-4.2
36101_s_at	M63978	634	Human vascular endothelial growth factor gene, exon 8.	8.0	203.5	298.4	191.3
31504_at	M64098	635	Human high density lipoprotein binding protein (HBP) mRNA, complete cds.	-1.5	1.6	-1.5	1.6
1457_at	M64174	636	Human protein-tyrosine kinase (JAK1) mRNA, complete cds.	-1.6	1.2	-1.1	-1.1
2016_s_at	M64241	637	Human Wilm's tumor-related protein (QM) mRNA, complete cds.	1.2	1.9	1.5	-1.3
32226_at	M64571	638	Human microtubule-associated protein 4 mRNA, complete cds.	2.5	-5.4	-1.8	-1.3
243_g_at	M64571	638	zo01b05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566385 3' similar to gb:M64571 MICROTUBULE-ASSOCIATED PROTEIN 4 (HUMAN);, mRNA sequence.	2.5	2.1	-1.7	1.7
32737_at	M64595	639	Human small G protein (Gx) mRNA, 3' end.	1.1	1.6	1.1	1.8
31573_at	M64716	640	Human ribosomal protein S25 mRNA, complete cds.	-1.9	-16.7	-1.4	-1.1
32207_at	M64925	641	Human palmitoylated erythrocyte membrane protein (MPP1) mRNA, complete cds.	-1.0	1.2	1.8	2.1
1383_at	M64929	642	Human protein phosphatase 2A alpha subunit mRNA, complete cds.	-2.0	1.3	1.2	-1.3
41167_at	M64929	642	Human protein phosphatase 2A alpha subunit mRNA, complete cds.	-2.0	2.1	3.4	1.6
37995_s_at	M67468	643	Human Fragile X mental retardation 1 FMR-1 gene, 3' end, clones BC72 and BC22.	-3.5	1.3	-3.7	-2.1
1792_g_at	M68520	644	aa08g07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812700 3' similar to gb:M68520 CELL DIVISION PROTEIN KINASE 2 (HUMAN);, mRNA sequence.	4.4	-2.3	4.5	6.8
1459_at	M68941	645	Human protein-tyrosine phosphatase mRNA, complete cds.	-1.5	6.2	1.0	1.0
33665_s_at	M73832	648	Human GM-CSF receptor (GM-CSF receptor) mRNA, complete cds.	-1.1	1.6	-1.3	-2.7
32183_at	M74002	649	Human arginine-rich nuclear protein mRNA, complete cds.	-2.8	3.6	-1.3	-2.2
37178_at	M74089	650	Human TB1 gene mRNA, 3' end.	1.4	10.2	3.0	3.3
31823_at	M74099	651	Human displacement protein (CCAAT) mRNA.	-2.1	1.1	-5.4	-5.4
39336_at	M74491	652	Human ADP-ribosylation factor 3 mRNA, complete cds.	1.2	-3.2	-2.3	-3.2
36729_g_at	M76446	653	Human alpha-A1-adrenergic receptor mRNA, complete cds.	1.0	3.6	2.3	3.0
32186_at	M80244	654	Human E16 mRNA, complete cds.	39.7	61.6	46.2	30.1
35017_f_at	M80469	656	Human MHC class I HLA-J gene, exons 1-8 and complete cds.	-1.0	1.3	-1.5	1.1
37027_at	M80899	657	Human novel protein AHNAK mRNA, partial sequence.	1.6	3.0	1.8	2.9
36773_f_at	M81141	658	Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds.	1.2	-1.1	-1.1	-1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
33551_s_at	M81778	662	Human serotonin 5-HT1C receptor mRNA, complete cds.	-1.2	-2.3	-2.3	2.1
37372_at	M81780	663	#N/A	4.9	1.0	6.1	7.0
40067_at	M82882	664	Human cis-acting sequence.	-5.5	-6.3	1.3	-1.8
32210_at	M83088	665	Human phosphoglucomutase 1 (PGM1) mRNA, complete cds.	-1.1	1.7	-1.5	1.6
570_at	M83221	666	Homo sapiens I-Rel mRNA, complete cds.	-1.1	4.8	3.3	4.3
1052_s_at	M83667	667	Human NF-IL6-beta protein mRNA, complete cds.	-24.3	-8.9	-19.6	-8.8
40739_at	M83670	668	Human carbonic anhydrase IV mRNA, complete cds.	-2.2	1.2	-2.1	-1.3
206_at	M84424	669	Human cathepsin E (CTSE) gene, exon 9 and complete cds.	4.2	3.4	1.0	1.0
40282_s_at	M84526	670	Human adipsin/complement factor D mRNA, complete cds.	-1.5	-1.3	-2.1	-1.5
37095_r_at	M84562	671	Human formyl peptide receptor-like receptor (FPRL1) mRNA, complete cds.	-1.8	2.9	1.2	1.6
1653_at	M84711	672	Human v-fos transformation effector protein (Fte-1), mRNA complete cds.	-1.6	-1.7	-1.8	-1.7
38666_at	M85169	673	Human homologue of yeast sec7 mRNA, complete cds.	-1.2	-2.5	-2.5	-10.8
32340_s_at	M85234	674	Human nuclease sensitive element binding protein-1 mRNA, complete cds.	1.1	3.3	3.1	2.7
1235_at	M86400	675	Human phospholipase A2 mRNA, complete cds.	1.0	3.4	2.3	2.1
571_at	M86667	676	H.sapiens NAP (nucleosome assembly protein) mRNA, complete cds.	-2.2	1.7	1.3	-3.0
39263_at	M87434	677	Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, complete cds.	1.0	5.0	2.0	3.6
38517_at	M87503	678	Human IFN-responsive transcription factor subunit mRNA, complete cds.	-1.5	1.1	1.1	-1.5
574_s_at	M87507	679	Human interleukin 1-beta converting enzyme isoform beta (IL1BCE) mRNA, complete cds.	-1.3	-1.8	-1.5	-2.3
39346_at	M88108	680	Human p62 mRNA, complete cds.	-1.7	2.1	1.2	1.0
38729_at	M88279	681	Human immunophilin (FKBP52) mRNA, complete cds.	1.8	10.9	4.2	1.0
41239_r_at	M90696	682	Human cathepsin S (CTSS) mRNA, complete cds.	1.1	-1.0	-1.5	1.3
38417_at	M91029	683	Human AMP deaminase (AMPD2) mRNA.	-3.2	-1.9	-3.3	-2.8
38585_at	M91036	684	#N/A	-1.7	7.5	1.0	1.2
35868_at	M91211	685	Human receptor for advanced glycosylation end products (RAGE) mRNA, partial cds.	1.4	-2.5	-5.6	-2.8
35225_at	M91592	686	Human zinc-finger protein (ZNF76) gene, partial cds.	6.3	1.0	1.8	1.0
40619_at	M91670	687	Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds.	6.8	7.0	4.5	2.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1795_g_at	M92287	688	zt76g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728304 3' similar to gb:M92287 G1/S-SPECIFIC CYCLIN D3 (HUMAN);, mRNA sequence.	-5.6	-6.6	-6.6	-7.5
1794_at	M92287	688	Homo sapiens cyclin D3 (CCND3) mRNA, complete cds.	-5.6	-5.2	-4.3	-3.5
31481_s_at	M92383	690	Homo sapiens thymosin beta-10 gene, 3'end.	-1.1	-2.0	-2.2	-2.1
33305_at	M93056	692	Human mononcyte/neutrophil elastase inhibitor mRNA sequence.	1.8	2.0	1.1	1.1
1463_at	M93425	693	Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds.	1.0	2.2	1.7	1.2
32553_at	M94046	694	Human zinc finger protein (MAZ) mRNA.	1.6	-1.0	-1.7	-1.0
33677_at	M94314	695	Homo sapiens ribosomal protein L30 mRNA, complete cds.	1.3	3.8	3.5	1.4
38016_at	M94630	696	Homo sapiens hnRNP-C like protein mRNA, complete cds.	-3.1	4.1	-1.2	1.4
39330_s_at	M95178	697	Human non-muscle alpha-actinin mRNA, complete cds.	1.3	-1.3	-1.6	-1.3
210_at	M95678	698	Homo sapiens phospholipase C-beta-2 mRNA, complete cds.	1.1	-2.9	-4.9	-4.2
1654_at	M95712	699	Human B-raf mRNA, complete cds.	2.4	5.2	1.3	-1.6
37855_at	M95767	700	Homo sapiens di-N-acetylchitobiase mRNA, complete cds.	-1.0	-1.3	-1.8	-3.8
36931_at	M95787	701	Human 22kDa smooth muscle protein (SM22) mRNA, complete cds.	-3.5	3.0	1.2	1.3
38782_at	M95809	702	Human basic transcription factor 62kD subunit (BTF2), complete cds.	-2.7	6.2	6.2	4.7
40817_at	M96824	703	Human nucleobindin precursor mRNA, complete cds.	2.3	-1.7	-2.6	-2.7
36517_at	M96982	704	Homo sapiens U2 snRNP auxiliary factor small subunit, complete cds.	-1.1	2.0	2.0	-1.3
1565_s_at	M96995	705	Human GRB2 isoform mRNA.	1.1	2.5	1.7	1.9
33855_at	M96995	705	Homo sapiens epidermal growth factor receptor-binding protein GRB2 (EGFRBP-GRB2) mRNA sequence.	1.1	1.2	-1.0	1.0
32621_at	M97388	706	Human TATA binding protein-associated phosphoprotein (DR1) mRNA, complete cds.	-2.3	-6.6	-2.4	-6.6
32860_g_at	M97935	707	Homo sapiens transcription factor ISGF-3 mRNA, complete cds.	-1.6	-1.0	-1.2	-3.4
39861_at	M98343	708	Homo sapiens amplaxin (EMS1) mRNA, complete cds.	1.0	25.4	2.0	13.6
38008_at	M98528	709	Homo sapiens neuron-specific protein gene, last exon, clone D4S234.	1.0	2.3	-1.0	1.5
41425_at	M98833	710	Homo sapiens ERGB transcription factor mRNA, complete cds.	2.4	-4.9	-4.4	-4.9
38234_at	M99438	711	Human transducin-like enhancer protein (TLE3) mRNA, complete cds.	-3.4	-1.2	1.1	1.3
40692_at	M99439	712	Human transducin-like enhancer protein (TLE4) mRNA, 3' end.	-1.6	-7.1	-4.0	-7.1
38317_at	M99701	713	Homo sapiens (pp21) mRNA, complete cds.	5.7	2.4	3.2	3.3
35841_at	N24355	714	#N/A	1.5	-1.2	1.2	1.1

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
34210_at	N90866	715	#N/A	1.1	-14.5	-1.7	-5.0
39798_at	R87876	716	#N/A	-1.3	1.1	1.6	1.2
33391_r_at	S57235	717	CD68=110kda transmembrane glycoprotein [human, promonocyte cell line U937, mRNA, 1722 nt].	4.4	1.0	9.4	6.5
33944_at	S60099	718	APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt].	1.0	1.5	1.3	1.1
39420_at	S62138	719	TLS/CHOP=hybrid gene {translocation breakpoint} [human, myxoid liposarcomas cells, mRNA Mutant, 1682 nt].	3.1	8.2	10.5	6.5
39180_at	S62140	720	TLS=translocated in liposarcoma [human, mRNA, 1824 nt].	1.1	1.6	1.5	1.6
872_i_at	S62539	721	insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt].	3.4	6.0	-1.2	-1.2
1785_at	S66431	722	RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].	-1.5	1.1	1.2	-4.0
32065_at	S68134	723	Homo sapiens cyclic AMP-responsive element modulator beta isoform (CREM) mRNA, complete cds.	1.0	13.7	20.3	7.6
32681_at	S68616	724	Na+/H+ exchanger NHE-1 isoform [human, heart, mRNA, 4516 nt].	2.2	2.1	1.8	1.9
32175_at	S72008	725	hCDC10=CDC10 homolog [human, fetal lung, mRNA, 2314 nt].	-1.9	-1.6	-2.4	-2.3
218_at	S74221	728	IK=IK factor [human, leukemic cells K562, chronic myeloid leukemia patient, mRNA, 756 nt].	-2.5	-1.4	-4.6	-3.1
545_g_at	S76638	729	p50-NF-kappa B homolog [human, peripheral blood T cells, mRNA, 3113 nt].	2.4	15.9	8.4	10.3
544_at	S76638	729	p50-NF-kappa B homolog [human, peripheral blood T cells, mRNA, 3113 nt].	2.4	29.4	17.3	16.1
37983_at	S77410	730	type 1 angiotensin II receptor [human, liver, mRNA, 2268 nt].	-1.9	8.0	-1.7	-1.7
37179_at	S77763	731	nuclear factor erythroid 2 isoform f=basic leucine zipper protein {alternatively spliced, exon 1f} [human, fetal liver, mRNA, 1678 nt].	-3.0	-90.4	-90.4	-22.4
37210_at	S78296	732	neurofilament-66 [human, fetal brain, mRNA, 3197 nt].	-2.2	4.6	3.1	6.4
36210_g_at	S78771	733	NAT=CpG island-associated gene [human, mRNA, 1741 nt].	1.2	2.5	1.6	-1.5
36209_at	S78771	733	NAT=CpG island-associated gene [human, mRNA, 1741 nt].	1.2	2.1	2.6	1.7
34570_at	S79522	734	ubiquitin carboxyl extension protein [human, mRNA, 540 nt].	-1.0	2.1	1.0	1.0
548_s_at	S80267	735	p72syk {G insertion nucleotide 92} [human, Jurkat E6-1 J.CaM1 cells, mRNA Partial Mutant, 1909 nt].	-6.2	-3.2	-2.6	-1.2
36447_at	S80990	736	ficolin [human, uterus, mRNA, 1736 nt].	-1.1	-2.2	-2.5	-2.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
223_at	S81003	737	L-UBC=ubiquitin conjugating enzyme [human, odontogenic keratocysts, mRNA Partial, 683 nt].	-1.6	-3.3	-7.8	-1.7
1237_at	S81914	738	IEX-1=radiation-inducible immediate-early gene [human, placenta, mRNA Partial, 1223 nt].	4.8	34.3	19.9	17.8
40714_at	S82198	739	caldecrin=serum calcium-decreasing factor [human, pancreas, mRNA Partial, 894 nt].	1.4	1.0	7.6	1.2
201_s_at	S82297	740	Human beta-2-microglobulin gene, exons 2 and 3.	4.4	-1.0	1.3	-1.4
858_at	S90469	742	cytochrome P450 reductase [human, placenta, mRNA Partial, 2403 nt].	-1.4	-15.0	-2.1	-2.4
32538_at	S95936	743	transferrin [human, liver, mRNA, 2347 nt].	5.6	3.0	1.2	2.6
40872_at	T57872	744	#N/A	-1.2	-1.9	-2.1	-6.9
40091_at	U00115	745	Human zinc-finger protein (bcl-6) mRNA, complete cds.	-1.4	-2.9	-1.2	-1.6
40252_g_at	U00943	747	Human clone A9A2BRB2 (CAC)n/(GTG)n repeat-containing mRNA.	8.9	1.9	1.2	-2.0
40251_at	U00943	747	Human clone A9A2BRB2 (CAC)n/(GTG)n repeat-containing mRNA.	8.9	1.0	1.3	1.0
38063_at	U00952	748	Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA.	-1.2	-1.5	-2.3	-6.1
32135_at	U00968	749	Human SREBP-1 mRNA, complete cds.	-3.4	-1.4	1.1	1.8
39058_at	U01147	750	Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds.	2.0	-9.5	-1.8	-4.1
41132_r_at	U01923	751	Human BTK region clone ftp-3 mRNA.	-1.9	1.2	1.3	1.1
38527_at	U02493	753	Human 54 kDa protein mRNA, complete cds.	-1.9	-1.5	1.1	-1.5
553_g_at	U02570	754	Human CDC42 GTPase-activating protein mRNA, partial cds.	-3.8	-2.9	-7.9	-4.2
38526_at	U02882	755	Human rolipram-sensitive 3',5'-cyclic AMP phosphodiesterase mRNA, complete cds.	1.0	13.3	3.2	3.3
41155_at	U03100	756	Human alpha2(E)-catenin mRNA, complete cds.	-1.5	-3.7	-1.5	-8.8
41156_g_at	U03100	756	Human alpha2(E)-catenin mRNA, complete cds.	-1.5	-2.7	-1.4	-8.1
2031_s_at	U03106	758	Human wild-type p53 activated fragment-1 (WAF1) mRNA, complete cds.	5.4	55.5	53.5	30.7
35000_at	U03398	759	Human receptor 4-1BB ligand mRNA, complete cds.	1.6	1.0	1.0	1.0
184_at	U03642	760	Human G protein-coupled receptor APJ gene, complete cds.	1.0	6.6	3.3	5.9
37980_at	U03644	761	Human recepin mRNA, complete cds.	-1.8	-2.6	-3.0	-1.8
36641_at	U03851	762	Human capping protein alpha mRNA, partial cds.	-3.9	-1.8	-2.1	-2.6
36327_at	U03884	763	Human inwardly rectifying K+ channel (ROMK1) mRNA, complete cds.	6.7	5.7	1.0	1.0
36270_at	U04343	764	Human CD86 antigen mRNA, complete cds.	3.3	5.4	1.3	1.8
1069_at	U04636	765	Human cyclooxygenase-2 (hCox-2) gene, complete cds.	12.2	6.9	8.1	1.3

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
185_at	U04840	766	Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds.	6.7	6.6	1.7	7.4
41091_at	U05237	767	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA, complete cds.	-3.7	-3.4	-1.1	-1.4
1796_s_at	U05681	768	Human B-cell lymphoma 3-encoded protein (bcl-3) mRNA, complete cds.	5.4	4.3	2.5	3.2
37747_at	U05770	769	Human annexin V (ANX5) gene, exon 13.	1.0	4.3	8.5	4.8
32100_r_at	U06088	771	Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.	-8.9	-2.2	-23.5	-23.5
519_g_at	U07132	772	zu09a06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731314 3' similar to TR:G555752 G555752 RLD-1. ;, mRNA sequence.	1.8	2.0	1.2	1.3
37911_at	U07158	773	Human syntaxin mRNA, complete cds.	1.6	4.5	5.1	3.7
520_at	U07358	774	Human protein kinase (zpk) mRNA, complete cds.	3.7	4.5	2.0	5.9
36880_at	U07736	775	Human quinone oxidoreductase2 (NQO2) gene, exon 7, complete cds.	-1.5	1.1	-4.6	-10.3
1710_s_at	U07804	777	Human topoisomerase I mRNA, complete cds.	2.8	16.7	4.5	1.6
1030_s_at	U07806	778	Human topoisomerase I mRNA, complete cds.	-1.8	3.8	2.7	1.8
865_at	U08316	779	Human insulin-stimulated protein kinase 1 (ISPK-1) mRNA, complete cds.	1.4	-2.6	-1.6	-4.8
38478_at	U08377	780	Human homolog of Drosophila splicing regulator suppressor-of-white-apricot mRNA, complete cds.	-2.8	1.2	-4.9	1.6
33068_f_at	U08854	781	Human UDP glucuronosyltransferase precursor (UGT2B15) mRNA, complete cds.	1.3	12.0	7.0	10.8
38236_at	U09002	782	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNR2A) mRNA, complete cds.	3.5	-1.1	-1.2	2.2
38397_at	U09196	783	Human 1.1 kb mRNA upregulated in retinoic acid treated HL-60 neutrophilic cells.	1.2	1.0	-3.9	1.4
1031_at	U09564	784	Human serine kinase mRNA, complete cds.	-1.4	2.3	1.5	-1.1
1637_at	U09578	785	Homo sapiens MAPKAP kinase (3pK) mRNA, complete cds.	-6.1	-15.5	-15.5	-6.8
39412_at	U09825	786	Human acid finger protein mRNA, complete cds.	-1.5	-1.4	-1.9	-8.4
41713_at	U09848	787	Human zinc finger protein (ZNF139) mRNA, partial cds.	-2.0	2.6	1.0	2.7
37998_at	U09877	788	Human helicase-like protein (HLP) mRNA, complete cds.	-5.1	-13.5	-13.5	-13.5
189_s_at	U09937	789	H.sapiens urokinase plasminogen activator surface receptor (uPAR) mRNA.	7.8	66.3	8.2	30.6
36358_at	U09953	790	Human ribosomal protein L9 mRNA, complete cds.	-1.5	-2.5	1.3	2.8
35974_at	U10485	791	Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds.	-4.2	-2.8	-4.3	-3.4
1924_at	U11791	792	Human cyclin H mRNA, complete cds.	-1.1	5.1	3.5	2.0
39029_at	U11861	793	Human G10 homolog (edg-2) mRNA, complete cds.	-1.0	-3.5	-3.5	-3.4
1353_g_at	U11870	794	Homo sapiens interleukin 8 receptor alpha (IL8RA) mRNA, complete cds.	-3.1	-7.1	-9.0	-8.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1352_at	U11870	794	Human interleukin-8 receptor type A (IL8RBA) gene, promoter and complete cds.	-3.1	-7.1	-6.6	-8.8
1033_g_at	U11872	795	Homo sapiens interleukin 8 receptor beta (IL8RB) mRNA, complete cds.	-1.7	-3.6	-6.6	-8.5
41143_at	U12022	796	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds.	-1.1	-2.2	-1.7	-12.4
33396_at	U12472	798	Human glutathione S-transferase (GST phi) gene, complete cds.	-6.5	-1.5	6.7	10.4
38963_i_at	U12707	799	Human Wiskott-Aldrich syndrome protein (WASP) mRNA, complete cds.	-2.0	-1.7	-2.6	-2.2
38964_r_at	U12707	799	Human Wiskott-Aldrich syndrome protein (WASP) mRNA, complete cds.	-2.0	-2.2	-2.9	-2.3
40659_at	U12767	800	Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds.	4.1	49.9	63.1	45.4
190_at	U12767	800	Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds.	4.1	47.7	52.2	31.9
1240_at	U13022	801	Human negative regulator of programmed cell death ICH-1S (Ich-1) mRNA, complete cds.	2.8	5.2	4.2	7.6
39320_at	U13697	802	Human interleukin 1-beta converting enzyme isoform beta (IL1BCE) mRNA, complete cds.	-1.3	-2.0	-1.7	-2.0
868_at	U13991	803	Human TATA-binding protein associated factor 30 kDa subunit (tafII30) mRNA, complete cds.	-1.6	-1.2	-2.0	-1.7
869_at	U14193	804	Human TFIIA gamma subunit mRNA, complete cds.	1.3	-3.2	-2.1	-3.2
1034_at	U14394	805	Human tissue inhibitor of metalloproteinases-3 mRNA, complete cds.	9.3	8.0	4.2	8.5
1035_g_at	U14394	805	Human tissue inhibitor of metalloproteinases-3 mRNA, complete cds.	9.3	2.4	5.4	-1.8
34693_at	U14550	806	Human sialyltransferase SThM (sthm) mRNA, complete cds.	1.1	-1.0	-2.4	-1.5
1241_at	U14603	807	Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence.	-1.2	-1.7	-2.0	-5.2
32436_at	U14968	808	Human ribosomal protein L27a mRNA, complete cds.	1.4	-2.2	-3.0	-2.6
31385_at	U14969	809	Human ribosomal protein L28 mRNA, complete cds.	-1.2	-1.2	-1.3	-1.1
31511_at	U14971	810	Human ribosomal protein S9 mRNA, complete cds.	-1.2	1.4	1.0	1.2
31568_at	U14972	811	Human ribosomal protein S10 mRNA, complete cds.	-6.2	-1.3	-2.7	-1.7
32060_at	U15173	812	Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2) mRNA, complete cds.	-3.1	-10.9	-1.6	1.6
34092_at	U15177	813	Human cosmid CRI-JC2015 at D10S289 in 10sp13.	1.8	1.0	1.0	1.0
528_at	U15590	814	Homo sapiens heat shock 17kD protein 3 (HSPB3) mRNA, complete cds.	1.0	2.2	-2.8	1.3
529_at	U15932	815	Human dual-specificity protein phosphatase mRNA, complete cds.	17.7	55.3	43.9	18.2
845_at	U16031	816	Human transcription factor IL-4 Stat mRNA, complete cds.	-2.8	-1.5	-1.5	-1.1
33135_at	U17566	817	Human 65 kDa hydrophobic protein mRNA, complete cds.	1.9	-3.2	-1.5	-1.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1640_at	U17714	818	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds.	3.6	3.0	1.1	-3.2
1712_s_at	U17743	819	Homo sapiens MAP kinase kinase 4 (MKK4) mRNA, complete cds.	-3.3	-3.9	-1.3	-3.9
35751_at	U17886	820	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 8, and complete cds.	1.0	-14.5	-2.6	-2.3
39378_at	U17999	821	#N/A	-1.4	1.1	-1.9	-1.8
192_at	U18062	822	Human TFIID subunit TAFII55 (TAFII55) mRNA, complete cds.	-1.1	1.9	1.8	1.0
34836_at	U18420	823	Human ras-related small GTP binding protein Rab5 (rab5) mRNA, complete cds.	1.1	-1.4	-2.0	-1.5
37240_at	U18937	824	Human histidyl-tRNA synthetase homolog (HO3) mRNA, complete cds.	-3.7	2.4	-3.5	1.4
1038_s_at	U19247	825	#N/A	-2.4	-1.1	1.2	-1.1
849_g_at	U19261	826	zu49g02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741362 3', mRNA sequence.	27.4	223.7	124.4	89.7
848_at	U19261	826	Homo sapiens Epstein-Barr virus-induced protein mRNA, complete cds.	27.4	20.7	8.9	10.8
37944_at	U19523	827	Human GTP cyclohydrolase I mRNA, complete cds.	4.2	28.8	34.5	17.9
38442_at	U19718	828	Human microfibril-associated glycoprotein (MFAP2) mRNA, complete cds.	1.0	1.9	2.7	2.6
1551_g_at	U19796	829	ze23d07.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359821 3', mRNA sequence.	-2.0	-16.7	-2.0	-6.1
35309_at	U20428	831	Human SNC19 mRNA sequence.	2.3	3.2	1.4	2.9
1357_at	U20657	832	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds.	1.5	1.3	1.0	-1.4
535_s_at	U20816	833	Human p80HT (p80HT/NKFB-2) mRNA, complete cds.	1.0	16.4	10.3	11.1
38220_at	U20938	834	Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete cds.	-1.5	-2.6	-2.7	-2.4
37057_s_at	U21092	835	Human CD40 receptor associated factor 1 (CRAF1) mRNA, complete cds.	2.6	20.5	13.6	23.1
36495_at	U21931	836	Human fructose-1,6-biphosphatase (FBP1) gene, exon 7, and complete cds.	-1.3	-2.9	-1.7	-2.1
1552_i_at	U22028	837	Human cytochrome P450 (CYP2A13) gene, complete cds.	-2.8	6.6	1.4	-1.8
1039_s_at	U22431	838	Human MOP1 mRNA, complete cds.	-1.1	5.4	5.0	2.4
39108_at	U22526	839	Human 2,3-oxidosqualene-lanosterol cyclase mRNA, complete cds.	1.7	2.8	2.6	3.0
40063_at	U22897	840	Homo sapiens nuclear domain 10 protein (ndp52) mRNA, complete cds.	-1.5	1.2	1.1	-1.6
1556_at	U23946	841	Human putative tumor suppressor (LUCA15) mRNA, complete cds.	-12.4	-2.2	-2.9	-5.0
36962_at	U24105	842	Homo sapiens coatomer protein (COPA) mRNA, complete cds.	-1.2	1.7	1.3	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1558_g_at	U24152	843	zp05a06.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595474 3' similar to SW:KPAK_RAT P35465 SERINE/THREONINE-PROTEIN KINASE PAK ;, mRNA sequence.	-1.3	1.0	1.4	-1.2
32337_at	U25789	844	Human ribosomal protein L21 mRNA, complete cds.	-1.4	-8.5	-1.1	-2.1
37541_at	U25956	845	Human P-selectin glycoprotein ligand (SELPLG) gene, exon 2, and complete cds.	-6.4	-3.4	-9.7	-8.9
33758_f_at	U25988	846	Human pregnancy-specific glycoprotein 13 (PSG13') mRNA, complete cds.	1.0	6.0	2.6	3.0
33508_at	U26398	847	Human inositol polyphosphate 4-phosphatase mRNA, complete cds.	5.3	-2.1	1.6	3.3
1041_at	U26403	848	Human receptor tyrosine kinase ligand LERK-7 precursor (EPLG7) mRNA, complete cds.	13.3	3.1	1.0	1.1
195_s_at	U28014	850	Human Ich-2 cysteine protease mRNA, complete cds.	-1.3	1.4	1.2	-1.7
41741_at	U28686	851	Human putative RNA-binding protein RNPL mRNA, complete cds.	-2.9	1.2	1.1	-1.4
32443_at	U28687	852	Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.	4.5	-1.4	-2.1	-1.1
33098_at	U28694	853	Human eosinophil CC chemokine receptor 3 mRNA, complete cds.	-2.5	-1.3	-1.7	-2.3
35653_at	U28963	854	Human Gps2 (GPS2) mRNA, complete cds.	-1.6	-2.4	-2.4	-2.6
493_at	U29171	855	Human casein kinase I delta mRNA, complete cds.	-1.0	3.5	2.4	2.1
36411_s_at	U29943	856	Human ELAV-like neuronal protein-2 Hel-N2 mRNA, complete cds.	1.0	3.4	1.9	2.8
37423_at	U30246	857	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds.	1.0	4.8	-2.1	3.2
36963_at	U30255	858	Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds.	-4.0	-3.8	-5.4	-5.0
40453_s_at	U30826	859	Human splicing factor SRp40-1 (SRp40) mRNA, complete cds.	-1.1	-5.6	-1.9	-1.8
37735_at	U31383	860	Human G protein gamma-10 subunit mRNA, complete cds.	1.1	-2.4	-2.2	-3.2
38381_at	U32315	861	Human syntaxin 3 mRNA, complete cds.	-1.1	1.9	2.1	1.1
34856_at	U32331	862	Homo sapiens RIG mRNA, complete cds.	1.0	3.8	-1.1	2.1
40653_at	U32439	863	Human regulator of G-protein signaling similarity (RGS7) mRNA, partial cds.	4.1	1.0	2.3	1.0
31845_at	U32645	864	Human myeloid elf-1 like factor (MEF) mRNA, complete cds.	1.0	1.3	1.3	1.2
497_at	U32680	865	Human CLN3 mRNA, complete cds.	-2.5	4.0	2.1	2.7
36472_at	U32849	866	Homo sapiens Nmi mRNA, complete cds.	-1.6	-2.4	-2.3	-2.6
199_s_at	U33052	867	protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].	-4.4	-1.2	-1.4	-1.4
36835_at	U33052	867	Human lipid-activated, protein kinase PRK2 mRNA, complete cds.	-4.4	-1.6	-1.5	1.3
2009_at	U33284	868	Human protein tyrosine kinase PYK2 mRNA, complete cds.	1.7	2.2	2.0	2.8
31900_at	U33429	869	human K+ channel beta 2 subunit mRNA, complete cds.	-2.2	1.7	20.7	42.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
35279_at	U33821	870	Homo sapiens tax1-binding protein TXBP151 mRNA, complete cds.	1.2	-1.6	-1.4	-1.6
498_at	U33821	870	Homo sapiens tax1-binding protein TXBP151 mRNA, complete cds.	1.2	1.8	-1.2	-2.7
33570_at	U34962	871	Human transcription factor HCSX (hCsx) mRNA, complete cds.	2.1	1.0	1.0	1.0
38402_at	U36336	872	Human lysosome-associated membrane protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	-4.6	-1.9	-1.2	1.1
38943_at	U36787	873	Human putative holocytochrome c-type synthetase mRNA, complete cds.	1.8	3.4	2.8	7.3
34650_at	U36798	874	Homo sapiens platelet cGI-PDE mRNA, complete cds.	3.1	1.0	1.0	1.0
33103_s_at	U37122	875	Human adducin gamma subunit mRNA, complete cds.	1.9	1.4	1.1	-2.4
39358_at	U37146	876	Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds.	-4.5	2.3	2.0	2.9
40786_at	U37352	877	Human protein phosphatase 2A B'alpha1 regulatory subunit mRNA, complete cds.	-1.1	-1.6	-4.0	-13.1
176_at	U37352	877	Human protein phosphatase 2A B'alpha1 regulatory subunit mRNA, complete cds.	-1.1	-5.1	-5.1	-5.1
41308_at	U37408	878	Homo sapiens phosphoprotein CtBP mRNA, complete cds.	-3.4	1.1	-3.2	-1.7
41309_g_at	U37408	878	Homo sapiens phosphoprotein CtBP mRNA, complete cds.	-3.4	-1.3	-2.4	-1.5
1715_at	U37518	879	Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds.	-1.5	-5.9	-16.6	-23.3
37956_at	U37519	880	Human aldehyde dehydrogenase (ALDH8) mRNA, complete cds.	1.0	2.7	4.4	1.0
39684_at	U37707	881	Human dlg3 mRNA, complete cds.	-2.0	5.5	1.2	5.9
832_at	U39317	882	Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.	1.3	1.6	-2.3	-1.5
504_at	U39318	883	Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds.	1.1	2.9	1.8	1.1
833_at	U40279	885	Human beta-2 integrin alphaD subunit (ITGAD) gene, exons 25-30, and partial cds.	2.6	4.0	2.1	1.7
35365_at	U40282	886	Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.	-1.4	1.6	-1.1	-1.2
1797_at	U40343	887	Human CDK inhibitor p19INK4d mRNA, complete cds.	2.1	-6.0	-16.9	-78.1
834_at	U40462	888	Human Ikaros/LyF-1 homolog (hlk-1) mRNA, complete cds.	-10.0	2.8	-1.0	2.6
40007_at	U40462	888	Human Ikaros/LyF-1 homolog (hlk-1) mRNA, complete cds.	-10.0	1.8	1.1	-6.2
38107_at	U40998	889	Human retinal protein (HRG4) mRNA, complete cds.	1.3	-1.0	-1.4	1.1
37650_at	U41315	890	Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence.	-6.3	-4.0	-6.9	-2.3
37022_at	U41344	891	Human prolargin (PRELP) gene, exon 3 and complete cds.	2.0	14.1	7.1	7.2
36973_at	U41371	892	Human spliceosome associated protein (SAP 145) mRNA, complete cds.	-1.2	-27.4	-5.6	-6.1
36996_at	U41635	893	Human OS-9 precurosor mRNA, complete cds.	-1.8	-1.2	-1.9	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
35316_at	U41654	894	Human adenovirus protein E3-14.7k interacting protein 1 (FIP-1) mRNA, complete cds.	1.2	-2.1	-3.2	-1.9
34346_at	U42412	895	Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.	-1.2	2.4	1.2	1.0
505_at	U43077	896	Human CDC37 homolog mRNA, complete cds.	-9.1	-2.3	-1.3	-2.6
38580_at	U43083	897	Human G alpha-q (Gaq) mRNA, complete cds.	-1.6	1.6	1.2	-1.4
836_at	U43148	898	Human patched homolog (PTC) mRNA, complete cds.	2.3	3.7	-1.3	-1.0
506_s_at	U43185	899	Homo sapiens signal transducer and activator of transcription (STAT5) mRNA, complete cds.	-1.2	1.1	-1.7	-1.3
40458_at	U43185	899	Human signal transducer and activator of transcription Stat5A mRNA, complete cds.	-1.2	6.0	2.5	2.3
507_s_at	U43189	900	Human Ets transcription factor (NERF-2) mRNA, complete cds.	-1.7	-7.1	-1.7	-1.3
39078_at	U43286	901	Human selenophosphate synthetase 2 (SPS2) mRNA, complete cds.	1.8	1.5	2.2	-1.2
33804_at	U43522	902	Human cell adhesion kinase beta (CAKbeta) mRNA, complete cds.	1.7	1.7	2.0	2.6
1991_s_at	U43784	903	Human mitogen activated protein kinase activated protein kinase-3 mRNA, complete cds.	1.0	-1.2	-2.1	-2.4
508_at	U43923	904	Human transcription factor SUPT4H mRNA, complete cds.	-1.4	-1.7	-1.8	-3.6
37252_at	U44755	905	Human PSE-binding factor PTF delta subunit mRNA, complete cds.	5.1	6.3	1.0	15.6
34774_at	U44772	906	Human palmitoyl protein thioesterase mRNA, complete cds.	1.1	-2.4	-1.2	-1.2
162_at	U44839	907	Human putative ubiquitin C-terminal hydrolase (UHX1) mRNA, complete cds.	1.7	3.8	2.0	2.0
36028_at	U45285	908	Human specific 116-kDa vacuolar proton pump subunit (OC-116KDa) mRNA, complete cds.	-1.5	-1.3	-1.2	1.0
33535_at	U45448	909	Human P2x1 receptor mRNA, complete cds.	-2.0	-3.7	-3.6	-1.7
41151_at	U45973	910	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds.	3.3	2.1	-1.6	1.5
37685_at	U45976	911	Human clathrin assembly protein lymphoid myeloid leukemia (CALM) mRNA, complete cds.	-1.9	-1.7	-1.5	-3.3
1524_at	U46194	912	Human renal cell carcinoma antigen RAGE-4 mRNA, complete putative cds.	4.9	2.7	1.4	2.9
35816_at	U46692	913	Human cystatin B gene, complete cds.	1.7	3.9	6.4	4.6
40898_at	U46751	914	Human phosphotyrosine independent ligand p62 for the Lck SH2 domain mRNA, complete cds.	1.3	5.7	8.0	6.0
36667_at	U47025	915	Human fetal brain glycogen phosphorylase B mRNA, complete cds.	-4.1	4.2	1.0	3.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
39165_at	U47101	916	Human NifU-like protein (hNifU) mRNA, partial cds.	-7.4	-4.2	-27.5	-8.1
1913_at	U47414	917	Human cyclin G2 mRNA, complete cds.	-2.1	-4.0	-3.6	-5.4
471_f_at	U47634	918	Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.	1.6	3.4	1.5	2.6
34003_at	U47924	920	#N/A	2.4	-1.5	-1.7	1.0
34405_at	U47927	921	Human isopeptidase T (ISOT) mRNA, complete cds.	1.0	-4.0	2.0	1.7
843_at	U48296	922	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds.	1.6	1.7	1.2	-1.2
844_at	U48707	923	Human protein phosphatase-1 inhibitor mRNA, complete cds.	2.0	1.6	-2.6	3.1
473_g_at	U48730	924	Human signal transducer and activator of transcription Stat5B mRNA, complete cds.	1.0	-5.3	-2.3	-1.3
32977_at	U49187	925	Human placenta (Diff48) mRNA, complete cds.	-2.1	-6.1	-6.2	-4.2
32978_g_at	U49187	925	Human placenta (Diff48) mRNA, complete cds.	-2.1	-15.1	-4.6	-4.1
37007_at	U49188	926	Human placenta (Diff33) mRNA, complete cds.	1.8	3.6	3.2	2.4
36959_at	U49278	927	Homo sapiens UEV-1 (UBE2V) mRNA, partial cds.	-3.2	-22.9	-3.7	-6.6
37011_at	U49392	928	Human allograft inflammatory factor-1 (AIF-1) mRNA, complete cds.	-1.2	-4.5	-1.4	-6.4
40396_at	U49395	929	Human ionotropic ATP receptor P2X5a mRNA, complete cds.	3.2	-1.3	1.7	-1.9
32153_s_at	U49869	930	Homo sapiens ubiquitin gene.	1.5	2.0	1.7	-1.8
41195_at	U49957	931	Human LIM protein (LPP) mRNA, partial cds.	-1.1	-3.5	-2.8	2.0
1718_at	U50523	932	Human BRCA2 region, mRNA sequence CG037.	-1.4	1.1	-1.2	-1.6
1532_g_at	U50535	933	zm91g11.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545348 3' similar to contains Alu repetitive element;, mRNA sequence.	-1.4	1.2	-1.8	-3.5
1008_f_at	U50648	934	Human interferon-inducible RNA-dependent protein kinase (Pkr) gene, exon 17 and complete cds.	-1.3	4.1	1.6	2.4
35364_at	U50939	935	Human amyloid precursor protein-binding protein 1 mRNA, complete cds.	4.5	-3.8	-3.8	-3.8
39749_at	U51007	936	Human 26S protease subunit S5a mRNA, complete cds.	1.1	-1.5	-2.0	-5.5
477_at	U51127	937	Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.	2.4	4.2	2.4	3.6
478_g_at	U51127	937	Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.	2.4	2.8	1.3	3.7
36465_at	U51127	937	Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.	2.4	-1.3	1.1	1.4
37759_at	U51240	938	Human lysosomal-associated multitransmembrane protein (LAPTm5) mRNA, complete cds.	-1.2	2.2	1.1	1.7
36372_at	U51333	939	Human hexokinase III (HK3) mRNA, complete cds.	-2.6	-1.7	-2.8	-2.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
36822_at	U51334	940	Human putative RNA binding protein (RBP56) mRNA, complete cds.	1.5	1.3	1.4	1.0
35755_at	U51336	941	Human inositol 1,3,4-trisphosphate 5/6-kinase mRNA, complete cds.	-1.7	-2.7	-5.6	-3.1
1647_at	U51903	942	Human RasGAP-related protein (IQGAP2) mRNA, complete cds.	-1.3	-1.7	-1.3	-1.1
37276_at	U51903	942	Human RasGAP-related protein (IQGAP2) mRNA, complete cds.	-1.3	2.0	-3.7	-4.5
38412_at	U53588	943	Homo sapiens MHC class 1 region.	1.1	3.3	1.7	1.6
35396_at	U54804	944	Human Has2 mRNA, complete cds.	5.0	1.0	1.0	1.0
32836_at	U56417	945	Human lysophosphatidic acid acyltransferase-alpha mRNA, complete cds.	-1.2	2.2	1.0	1.5
40910_at	U56637	946	Human capping protein alpha subunit isoform 1 mRNA, complete cds.	1.2	1.2	1.3	-1.2
171_at	U56833	947	Human VHL binding protein-1 (VBP-1) mRNA, partial cds.	1.8	-2.7	-1.2	1.5
806_at	U56998	948	Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds.	7.2	11.2	10.1	7.7
809_at	U57094	949	Human small GTP-binding protein mRNA, complete cds.	-2.0	1.1	-1.1	-1.8
38164_at	U57629	950	Human retinitis pigmentosa GTPase regulator (RPGR) mRNA, complete cds.	1.6	1.4	1.6	1.2
172_at	U57650	951	Human SH2-containing inositol 5-phosphatase (hSHIP) mRNA, complete cds.	-1.2	-7.2	-4.5	-8.0
33628_g_at	U57843	952	Human phosphatidylinositol 3-kinase delta catalytic subunit mRNA, complete cds.	1.3	-3.5	-3.5	-3.5
484_at	U59302	953	Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds.	1.2	-1.2	-1.9	-3.5
41260_at	U59321	954	Human DEAD-box protein p72 (P72) mRNA, complete cds.	1.2	-5.4	-1.4	-12.2
39742_at	U59863	955	Human TRAF-interacting protein I-TRAF mRNA, complete cds.	-4.4	2.7	2.9	-3.3
33371_s_at	U59877	956	Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds.	-7.8	-1.6	-2.4	-1.8
34670_at	U60899	957	Human lysosomal alpha-mannosidase (manB) gene, exon 24, 3' flanking region and complete cds.	-1.1	-6.6	-4.1	1.0
31855_at	U61374	958	Human novel protein with short consensus repeats of six cysteines mRNA, complete cds.	2.0	2.7	1.6	4.2
35018_at	U61538	959	Human calcium-binding protein chp mRNA, complete cds.	-1.4	4.0	1.7	3.0
40006_at	U63090	960	Human Gal beta-1,3 GalNAc alpha-2,3 sialyltransferase (ST3Gal II) mRNA, complete cds.	8.8	-2.4	-1.1	4.6
40974_at	U63541	961	Human mRNA expressed in HC/HCC livers and MolT-4 proliferating cells, partial sequence.	3.0	3.6	1.7	2.1
467_at	U63717	962	Homo sapiens osteoclast stimulating factor mRNA, complete cds.	-1.1	-4.4	-1.9	-4.4
810_at	U64105	963	Human guanine nucleotide exchange factor p115-RhoGEF mRNA, partial cds.	-1.6	-1.8	-3.1	-2.9
40385_at	U64197	964	Homo sapiens chemokine exodus-1 mRNA, complete cds.	72.0	50.3	57.9	13.2

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
1534_at	U64198	965	Human Il-12 receptor beta2 mRNA, complete cds.	4.2	1.0	1.0	5.7
811_at	U64444	966	Homo sapiens ubiquitin fusion-degradation 1 like protein (UFD1L) mRNA, complete cds.	-1.2	-3.2	-1.9	-2.6
35784_at	U64520	967	Human synaptobrevin-3 mRNA, complete cds.	-2.1	-1.7	-2.1	-2.1
34876_at	U65090	968	Human carboxypeptidase D mRNA, complete cds.	1.7	3.2	3.9	2.4
33863_at	U65785	969	Human 150 kDa oxygen-regulated protein ORP150 mRNA, complete cds.	-1.5	11.5	1.5	5.7
32104_i_at	U66063	970	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA, partial cds.	-1.2	-1.6	-2.2	-2.6
32105_f_at	U66063	970	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA, partial cds.	-1.2	-30.3	-30.3	-30.3
32459_at	U66088	971	Human sodium iodide symporter mRNA, complete cds.	5.1	1.0	1.0	1.0
138_at	U66464	972	Human hematopoietic progenitor kinase (HPK1) mRNA, complete cds.	4.9	4.3	2.5	1.5
452_at	U66615	973	Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA, complete cds.	-3.3	5.5	1.5	2.4
457_s_at	U67122	975	Human sentrin mRNA, complete cds.	-1.9	2.1	1.2	-4.2
1327_s_at	U67156	976	zf57d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381047 3', mRNA sequence.	2.6	-8.3	-2.5	-3.2
35695_at	U67615	977	Human beige protein homolog (chs) mRNA, complete cds.	-2.7	-3.8	-2.9	-3.2
35792_at	U67963	978	Human lysophospholipase homolog (HU-K5) mRNA, complete cds.	1.4	4.5	1.0	1.0
34759_at	U68494	979	Human hbc647 mRNA sequence.	1.3	4.6	-2.2	1.4
36938_at	U70063	980	Human acid ceramidase mRNA, complete cds.	1.1	1.1	1.1	1.4
461_at	U70063	980	Human acid ceramidase mRNA, complete cds.	1.1	1.2	1.0	-1.3
39424_at	U70321	981	Human herpesvirus entry mediator mRNA, complete cds.	1.4	2.0	2.3	2.2
38369_at	U70451	982	Human myleoid differentiation primary response protein MyD88 mRNA, complete cds.	-1.9	1.5	-1.1	1.3
41776_at	U70660	983	Human copper transport protein HAH1 (HAH1) mRNA, complete cds.	1.0	1.4	-1.2	1.3
34817_s_at	U70671	984	Human ataxin-2 related protein mRNA, partial cds.	1.5	-2.0	-1.3	-1.3
40138_at	U70735	985	Homo sapiens 34 kDa Mov34 homolog mRNA, complete cds.	-1.1	-1.3	-2.6	-1.3
34438_at	U71364	986	Human serine proteinase inhibitor (P19) mRNA, complete cds.	8.6	14.1	6.7	8.4
35227_at	U72066	987	Homo sapiens CtBP interacting protein CtIP (CtIP) mRNA, complete cds.	2.8	5.7	1.2	4.5
40100_at	U72206	988	Human guanine nucleotide regulatory factor (LFP40) mRNA, complete cds.	1.6	1.7	1.3	1.4
817_at	U72209	989	Human YY1-associated factor 2 (YAF2) mRNA, complete cds.	-1.4	1.7	-2.7	-3.1
37364_at	U72511	990	Human B-cell receptor associated protein (hBAP) mRNA, partial cds.	-3.3	1.5	-11.0	-4.0

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
33710_at	U72515	991	Human C3f mRNA, complete cds.	1.9	1.0	2.1	1.0
39147_g_at	U72936	993	Homo sapiens putative DNA dependent ATPase and helicase (ATRX) mRNA, alternatively spliced product 1, complete cds.	2.0	-2.3	-2.1	-1.4
38118_at	U73377	994	Human p66shc (SHC) mRNA, complete cds.	1.1	-1.0	-1.3	-1.7
37034_at	U73477	995	Human acidic nuclear phosphoprotein pp32 mRNA, complete cds.	-1.2	-1.1	-1.7	-2.4
33149_at	U73524	996	Human putative ATP/GTP-binding protein (HEAB) mRNA, complete cds.	-3.1	-3.2	-3.9	-3.9
39984_g_at	U73704	997	Homo sapiens 48 kDa FKBP-associated protein FAP48 mRNA, complete cds.	1.0	1.6	1.0	-1.0
41785_at	U73824	998	Human p97 mRNA, complete cds.	-3.3	-1.4	-1.9	-2.0
36913_at	U75679	999	Human histone stem-loop binding protein (SLBP) mRNA, complete cds.	-1.6	-4.4	-3.8	-4.4
37972_at	U75744	1000	Homo sapiens DNase gamma mRNA, complete cds.	2.2	4.3	2.9	4.2
38614_s_at	U77413	1001	Human O-linked GlcNAc transferase mRNA, complete cds.	-1.2	1.3	-2.1	-1.2
1633_g_at	U77735	1003	Human pim-2 protooncogene homolog pim-2h mRNA, complete cds.	2.3	2.8	1.5	1.4
1652_at	U77735	1003	Human pim-2 protooncogene homolog pim-2h mRNA, complete cds.	2.3	4.3	1.9	1.6
35414_s_at	U77914	1004	Human soluble protein Jagged mRNA, partial cds.	1.0	1.7	-3.2	2.6
466_at	U77948	1005	Human Bruton's tyrosine kinase-associated protein-135 mRNA, complete cds.	-3.1	-16.2	-8.6	-5.8
34348_at	U78095	1006	Homo sapiens placental bikunin mRNA, complete cds.	-3.2	-1.4	-2.4	1.2
38104_at	U78302	1007	Human 2,4-dienoyl-CoA reductase gene, exon 10 and complete cds.	-7.1	-8.5	-8.5	-8.5
1229_at	U78556	1008	Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds.	8.5	1.8	-1.6	-1.6
1230_g_at	U78556	1008	zw66a06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781138 3', mRNA sequence.	8.5	1.0	1.2	1.0
32852_at	U78678	1009	Human thioredoxin mRNA, nuclear gene encoding mitochondrial protein, complete cds.	8.4	1.0	1.0	1.0
35183_at	U78735	1010	Human ABC3 mRNA, complete cds.	4.2	11.4	5.3	1.0
41006_at	U79265	1011	Human clone 23614 mRNA sequence.	1.2	1.2	-2.0	-1.9
34371_at	U79267	1012	Human clone 23840 mRNA, partial cds.	-2.6	-2.6	-1.7	-3.0
32059_at	U79282	1013	Human clone 23801 mRNA sequence.	-7.6	-6.0	-2.1	-6.0
40955_at	U79287	1014	Human clone 23867 mRNA sequence.	-3.2	-1.9	-4.2	-3.2
35564_at	U79300	1015	Human clone 23629 mRNA sequence.	1.0	1.0	1.0	6.0
37875_at	U79725	1016	Human A33 antigen precursor mRNA, complete cds.	1.1	2.0	-5.4	1.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
34095_f_at	U80114	1017	Human immunoglobulin heavy chain variable region (V4-31) gene, partial cds.	1.0	13.9	-1.0	5.0
34307_at	U81006	1018	Human p76 mRNA, complete cds.	-4.0	-12.9	-10.9	-12.9
33901_at	U81375	1019	Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds.	1.1	-14.7	-14.7	-14.7
32113_at	U83115	1020	Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds.	-4.8	-1.7	-1.7	-1.7
40452_at	U83246	1021	Homo sapiens copine I mRNA, complete cds.	-1.6	-1.1	-2.7	-2.7
34749_at	U83461	1022	Human putative copper uptake protein (hCTR2) mRNA, complete cds.	-3.7	-1.2	-2.7	-1.4
38252_s_at	U84007	1023	Human glycogen debranching enzyme isoform 1 (AGL) mRNA, alternatively spliced isoform, complete cds.	3.3	1.0	1.0	3.4
38253_at	U84011	1024	Human glycogen debranching enzyme isoform 6 (AGL) mRNA, alternatively spliced isoform, complete cds.	3.3	1.8	-2.2	-2.2
32757_at	U84720	1025	Homo sapiens mRNA export protein (RAE1) mRNA, complete cds.	-9.5	1.2	-1.6	-1.6
1020_s_at	U85611	1026	Human Snk interacting protein 2-28 mRNA, complete cds.	-1.5	1.5	-1.1	-1.6
33637_g_at	U87459	1027	Human autoimmunogenic cancer/testis antigen NY-ESO-1 mRNA, complete cds.	3.6	2.1	1.0	1.5
33636_at	U87459	1027	Human autoimmunogenic cancer/testis antigen NY-ESO-1 mRNA, complete cds.	3.6	1.0	2.2	3.4
39182_at	U87947	1028	Human hematopoietic neural membrane protein (HNMP-1) mRNA, complete cds.	1.2	2.1	1.7	1.9
35913_at	U88047	1029	Homo sapiens DNA binding protein homolog (DRIL1) mRNA, complete cds.	1.0	1.7	-1.8	1.1
40606_at	U88629	1030	Human RNA polymerase II elongation factor ELL2, complete cds.	1.9	21.8	9.0	8.8
148_at	U88629	1030	Human RNA polymerase II elongation factor ELL2, complete cds.	1.9	7.1	4.3	7.2
33304_at	U88964	1031	Human HEM45 mRNA, complete cds.	-1.1	4.1	2.4	2.0
36960_at	U89278	1032	Human polyhomeotic 2 homolog (HPH2) mRNA, complete cds.	-4.2	-71.7	-11.3	-10.8
38542_at	U89322	1033	Homo sapiens nucleophosmin phosphoprotein (NPM) gene, 3' flanking sequence.	1.4	1.4	2.7	1.7
35351_at	U89505	1034	Human Hlark mRNA, complete cds.	-3.9	-5.1	-2.0	-2.0
35714_at	U89606	1035	Human pyridoxal kinase mRNA, complete cds.	1.2	3.9	3.6	4.1
447_g_at	U89896	1036	af16e12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031854 3' similar to TR:G854735 G854735 CASEIN KINASE 1 GAMMA 2 ISOFORM. ;, mRNA sequence.	1.7	1.3	-4.5	-11.4
446_at	U89896	1036	Homo sapiens casein kinase I gamma 2 mRNA, complete cds.	1.7	1.1	1.1	-1.0
32673_at	U90543	1038	Human butyrophilin (BTF1) mRNA, complete cds.	-7.9	-1.4	-1.7	-2.6
38760_f_at	U90546	1039	Human butyrophilin (BTF4) mRNA, complete cds.	-4.6	-7.1	-2.8	-2.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
35341_at	U90547	1040	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA, complete cds.	1.7	5.0	2.4	-1.0
34308_at	U90551	1041	Human histone 2A-like protein (H2A/l) mRNA, complete cds.	-3.0	-5.9	-4.6	-4.3
32629_f_at	U90552	1042	Human butyrophilin (BTF5) mRNA, complete cds.	-3.2	-3.2	-5.5	-3.0
35950_at	U90841	1043	Homo sapiens SSX4 (SSX4) mRNA, complete cds.	1.2	-1.4	1.0	1.9
40787_at	U90911	1044	Human clone 23652 mRNA sequence.	-1.9	1.8	1.3	-1.6
38411_at	U90916	1045	Human clone 23815 mRNA sequence.	-1.5	-2.8	-2.8	-3.7
41475_at	U91512	1046	Human adhesion molecule ninjurin mRNA, complete cds.	1.5	4.6	2.5	3.4
38074_at	U91932	1048	Homo sapiens AP-3 complex sigma3A subunit mRNA, complete cds.	-2.3	-1.0	-2.4	-2.1
32047_at	U91985	1049	Human DNA fragmentation factor-45 mRNA, complete cds.	4.1	1.0	1.0	1.0
31876_r_at	U92014	1050	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence.	11.7	1.0	2.7	1.0
1434_at	U92436	1051	Human mutated in multiple advanced cancers protein (MMAC1) mRNA, complete cds.	-1.9	-1.0	-2.7	-1.5
39552_at	U92436	1051	Human mutated in multiple advanced cancers protein (MMAC1) mRNA, complete cds.	-1.9	-1.8	-2.1	-1.3
37326_at	U93305	1052	#N/A	-1.7	-1.1	-1.7	-2.3
35036_at	U94333	1053	Human Clq/MBL/SPA receptor C1qR(p) mRNA, complete cds.	2.0	4.7	3.5	5.0
37591_at	U94592	1054	Human uncoupling protein homolog (UCPH) mRNA, complete cds.	1.4	-3.4	-2.3	-2.0
33859_at	U96915	1055	Homo sapiens sin3 associated polypeptide p18 (SAP18) mRNA, complete cds.	-2.5	-1.1	-1.3	-2.7
33506_at	U96919	1056	Homo sapiens inositol polyphosphate 4-phosphatase type I-beta mRNA, complete cds.	5.3	1.9	-1.0	-5.5
33507_g_at	U96919	1056	Homo sapiens inositol polyphosphate 4-phosphatase type I-beta mRNA, complete cds.	5.3	1.6	1.0	1.0
428_s_at	V00567	1057	Human beta-2-microglobulin gene, exons 2 and 3.	2.4	2.0	1.7	1.4
37677_at	V00572	1058	Human mRNA encoding phosphoglycerate kinase.	-1.3	1.8	1.9	1.3
32603_at	W27118	1060	#N/A	-1.9	1.2	1.2	1.9
32004_s_at	W32483	1061	#N/A	-6.2	1.5	1.4	1.3
34317_g_at	W52024	1062	#N/A	-1.5	-4.7	-2.8	-1.9
38087_s_at	W72186	1063	#N/A	-1.1	-2.8	-2.9	-8.9
41471_at	W72424	1064	#N/A	-2.0	1.2	-1.5	1.1
40541_at	X01630	1065	Human mRNA for argininosuccinate synthetase.	2.7	1.4	-1.0	1.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
36781_at	X01683	1066	Human alpha-1-antitrypsin mRNA, complete cds.	1.8	2.5	1.4	1.4
40567_at	X01703	1067	Human gene for alpha-tubulin (b alpha 1).	-2.1	1.1	-1.1	-1.5
41485_at	X02152	1068	Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27).	2.8	3.0	2.2	1.7
35315_at	X02544	1069	Human mRNA for alpha1-acid glycoprotein (orosomucoid).	1.9	1.5	1.3	-1.5
32276_at	X03342	1070	Human mRNA for ribosomal protein L32.	-1.5	-1.3	-1.2	-1.3
1334_s_at	X03656	1071	Human mRNA for granulocyte colony-stimulating factor (G-CSF) (pBRV-2).	16.4	-4.0	-4.0	-4.0
37975_at	X04011	1072	Human mRNA of X-CGD gene involved in chronic granulomatous disease located on chromosome X.	1.8	-3.3	-3.3	-3.3
36138_at	X04106	1074	Human mRNA for calcium dependent protease (small subunit).	1.4	-23.7	-14.5	-4.7
33908_at	X04366	1075	Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).	3.3	-8.8	-15.8	-8.9
32612_at	X04412	1076	Human mRNA for plasma gelsolin.	-1.6	-6.0	-2.9	-3.9
33341_at	X04526	1077	Human liver mRNA for beta-subunit signal transducing proteins Gs/Gi (beta-G).	-1.6	-1.1	-1.2	-1.5
1323_at	X04803	1078	Homo sapiens ubiquitin gene.	1.5	1.6	1.4	-2.2
37307_at	X04828	1079	Human mRNA for G(i) protein alpha-subunit (adenylate cyclase inhibiting GTP-binding protein).	1.4	-2.1	-3.2	-2.0
32336_at	X05236	1080	Human fibroblast mRNA for aldolase A.	-2.0	-1.2	-1.8	-1.1
33866_at	X05276	1081	Human mRNA for fibroblast tropomyosin TM30 (pI).	1.4	8.4	6.5	3.4
37403_at	X05908	1082	Human mRNA for lipocortin.	-1.2	2.4	1.7	-2.1
36679_at	X06272	1084	Human mRNA for docking protein (signal recognition particle receptor).	-3.0	1.4	-1.8	-1.5
1976_s_at	X06292	1085	Human c-fes/fps proto-oncogene.	2.0	-3.7	-23.1	-23.1
1336_s_at	X06318	1086	Human mRNA for protein kinase C (PKC) type beta I.	-5.9	-8.4	-2.4	-2.7
38743_f_at	X06409	1087	Human mRNA fragment for activated c-raf-1 (exons 8-17).	-2.4	-8.0	-6.0	-6.1
1337_s_at	X06614	1088	Human mRNA for retinoic acid receptor.	-1.3	1.1	1.3	1.8
32330_at	X06617	1089	Human mRNA for ribosomal protein S11.	-1.3	-1.3	-1.3	-4.0
36661_s_at	X06882	1090	Human gene for CD14 differentiation antigen.	-3.5	2.3	1.6	2.2
36591_at	X06956	1091	Human HALPHA44 gene for alpha-tubulin, exons 1-3.	-2.5	-2.9	-3.2	-2.5
1217_g_at	X07109	1092	Human mRNA for protein kinase C (PKC) type beta I.	-1.1	-1.3	-1.3	1.2
37582_at	X07696	1093	Human mRNA for cytokeratin 15.	1.0	2.6	5.1	11.6
34666_at	X07834	1095	Human mRNA for manganese superoxide dismutase (EC 1.15.1.1).	5.7	16.5	15.9	6.7

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38119_at	X12496	1097	Human mRNA for erythrocyte membrane sialoglycoprotein beta (glycophorin C).	1.0	2.8	1.8	3.2
985_s_at	X12830	1098	Human mRNA for interleukin-6-receptor.	1.3	-1.6	1.2	3.3
39239_at	X13444	1099	Human mRNA for CD8 beta-chain glycoprotein (CD8 beta.1).	5.0	18.2	31.0	16.3
41231_f_at	X13546	1100	Human HMG-17 gene for non-histone chromosomal protein HMG-17.	-1.0	1.4	-1.7	-1.1
37033_s_at	X13710	1101	H.sapiens unspliced mRNA for glutathione peroxidase.	1.0	2.1	2.1	2.9
33820_g_at	X13794	1102	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS).	-5.3	2.7	2.2	1.1
37180_at	X14034	1103	Human mRNA for phospholipase C.	-1.3	-1.1	-1.7	-1.7
31870_at	X14046	1104	Human mRNA for leukocyte antigen CD37.	1.2	-3.1	-2.8	-2.3
38610_s_at	X14487	1105	Human gene for acidic (type I) cytokeratin 10.	1.0	1.0	-2.7	-1.6
40415_at	X14813	1106	Human liver mRNA for 3-oxoacyl-CoA thiolase.	-5.3	-30.8	-5.7	-3.1
33480_at	X15393	1108	H.sapiens motilin gene exon 2 (and joined CDS).	2.2	2.6	2.0	2.0
33676_at	X15940	1109	Human mRNA for ribosomal protein L31.	-1.0	-1.2	-1.4	1.4
1220_g_at	X15949	1110	Human mRNA for interferon regulatory factor-2 (IRF-2).	-4.5	1.1	-2.5	-1.4
1219_at	X15949	1110	Human mRNA for interferon regulatory factor-2 (IRF-2).	-4.5	-18.4	-16.7	-18.4
35201_at	X16135	1112	Human mRNA for novel heterogeneous nuclear RNP protein, L protein.	1.9	2.0	-1.1	-1.1
1919_at	X16316	1113	Human mRNA for vav oncogene.	-1.4	-1.1	-6.1	-1.4
988_at	X16354	1114	Human mRNA for transmembrane carcinoembryonic antigen BGPa (formerly TM1-CEA).	1.2	-2.0	1.4	-6.1
37021_at	X16832	1116	Human mRNA for cathepsin H (EC 3.4.22.16).	-4.3	1.5	-2.4	-1.5
36985_at	X17025	1117	Human homolog of yeast IPP isomerase.	1.0	-2.5	-1.6	-1.7
35338_at	X17094	1119	Human fur mRNA for furin.	-5.4	-13.2	-13.2	-13.2
31527_at	X17206	1120	Human mRNA for LLRep3.	-1.1	-2.3	-2.8	-1.7
32786_at	X51345	1121	Human jun-B mRNA for JUN-B protein.	3.4	1.7	1.4	-1.6
35251_at	X51435	1122	Human PRDII-BF1 gene for a DNA-binding protein.	-6.2	6.1	7.6	4.3
40103_at	X51521	1123	Human mRNA for ezrin.	2.8	3.2	1.5	2.0
35965_at	X51757	1124	Human heat-shock protein HSP70B' gene.	-10.9	-4.9	-4.0	-7.3
117_at	X51757	1124	Human heat-shock protein HSP70B' gene.	-10.9	-10.9	-5.4	-3.1
38515_at	X51801	1125	Human OP-1 mRNA for osteogenic protein.	1.0	4.0	1.0	7.7
788_s_at	X52001	1126	Human endothelin 3 (EDN3) mRNA, complete cds.	2.0	1.0	1.0	10.8

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37603_at	X52015	1127	H.sapiens mRNA for interleukin-1 receptor antagonist.	32.8	37.3	22.6	19.4
1341_at	X52056	1128	Human mRNA for spi-1 proto-oncogene.	1.2	1.7	-1.0	1.3
34647_at	X52104	1129	Human mRNA for p68 protein.	1.9	2.0	2.3	-1.0
37963_at	X52151	1130	Homo sapiens arylsulphatase A mRNA, complete cds.	-1.0	-8.3	-8.3	-8.3
32888_at	X52213	1131	H.sapiens Itk mRNA.	11.8	6.4	3.4	6.2
404_at	X52425	1132	Human IL-4-R mRNA for the interleukin 4 receptor.	-1.5	1.1	-1.8	-1.5
32352_at	X52730	1135	Human gene for phenylethanolamine N-methylase (PNMT) (EC 2.1.1.28).	1.6	2.4	3.1	2.9
405_at	X52773	1136	Human mRNA for retinoic acid receptor-like protein.	-13.4	-2.6	-2.3	1.0
33667_at	X52851	1137	Human cyclophilin gene for cyclophilin (EC 5.2.1.8).	-12.8	2.2	1.6	1.2
35055_at	X53281	1138	H.sapiens BTF3b mRNA.	-1.3	1.3	1.4	2.0
38027_at	X53742	1139	H.sapiens mRNA for fibulin-1 B.	2.7	1.9	1.6	4.1
32440_at	X53777	1140	Human L23 mRNA for putative ribosomal protein.	-2.9	-1.1	-2.4	-5.4
32916_at	X54134	1141	Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon.	1.9	5.4	5.5	2.9
33447_at	X54304	1142	Human mRNA for myosin regulatory light chain.	-1.1	1.3	1.2	-1.5
993_at	X54637	1143	Human tyk2 mRNA for non-receptor protein tyrosine kinase.	-1.8	-20.3	-4.4	-2.1
793_at	X54936	1144	H.sapiens mRNA for placenta growth factor (PlGF).	4.5	18.8	1.0	8.2
31816_at	X55079	1145	Human lysosomal alpha-glucosidase gene exon 1.	-2.3	-34.1	-9.5	-1.4
34645_at	X55715	1146	Human Humss3 mRNA for 40S ribosomal protein s3.	-1.0	-1.2	-1.9	-2.2
32394_s_at	X55954	1147	Human mRNA for HL23 ribosomal protein homologue.	-1.4	2.0	1.7	1.2
32395_r_at	X55954	1147	Human mRNA for HL23 ribosomal protein homologue.	-1.4	-12.9	1.1	-12.9
36766_at	X55988	1148	Human EDN mRNA for eosinophil derived neurotoxin.	1.2	-7.5	-3.2	-1.3
37448_s_at	X56009	1149	Human GSA mRNA for alpha subunit of GsGTP binding protein.	-1.5	-1.9	-3.0	-2.3
409_at	X56468	1150	Human mRNA for 14.3.3 protein, a protein kinase regulator.	-4.4	-1.0	-1.2	1.1
41483_s_at	X56681	1151	Human junD mRNA.	-1.1	-2.1	-2.4	-2.1
1612_s_at	X56681	1151	Human jun-D mRNA for JUN-D protein.	-1.1	-2.1	-2.5	-2.3
41484_r_at	X56681	1151	Human junD mRNA.	-1.1	1.4	-3.8	1.2
35119_at	X56932	1153	H.sapiens mRNA for 23 kD highly basic protein.	-1.0	-2.2	-2.3	-2.4
1501_at	X57025	1154	Human IGF-I mRNA for insulin-like growth factor I.	6.3	4.4	1.0	1.0
38737_at	X57025	1154	Human IGF-I mRNA for insulin-like growth factor I.	6.3	1.0	1.0	1.0
410_s_at	X57152	1155	Human casein kinase II beta subunit mRNA, complete cds.	-1.8	-1.0	-1.7	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37272_at	X57206	1156	H.sapiens mRNA for 1D-myo-inositol-trisphosphate 3-kinase B isoenzyme.	-4.7	-2.5	-2.2	1.2
32324_at	X57346	1157	H.sapiens mRNA for HS1 protein.	-1.6	-1.1	-1.3	-1.6
411_i_at	X57351	1158	Human 1-8D gene from interferon-inducible gene family.	3.3	1.1	-2.7	-1.5
40153_at	X57522	1159	H.sapiens RING4 cDNA.	-1.0	1.0	-2.4	-1.3
36333_at	X57958	1160	H.sapiens mRNA for ribosomal protein L7.	-5.8	1.7	1.6	2.5
33352_at	X57985	1161	H.sapiens genes for histones H2B.1 and H2A.	1.4	1.6	1.5	1.8
40511_at	X58072	1162	Human hGATA3 mRNA for trans-acting T-cell specific transcription factor.	1.8	1.0	1.0	2.7
32145_at	X58141	1163	Human mRNA for erythrocyte adducin alpha subunit.	-5.0	-3.3	-2.4	-2.0
37381_g_at	X59268	1164	Human mRNA for general transcription factor IIB.	-3.1	1.6	-2.9	-3.8
38521_at	X59350	1165	H.sapiens mRNA for B cell membrane protein CD22.	1.0	-1.7	2.5	3.8
36122_at	X59417	1167	H.sapiens PROS-27 mRNA.	1.1	2.4	1.2	1.7
998_s_at	X59770	1168	H.sapiens IL-1R2 mRNA for type II interleukin-1 receptor, (cell line CB23).	-1.1	8.1	3.7	2.6
999_at	X59812	1169	H.sapiens CYP 27 mRNA for vitamin D3 25-hydroxylase.	-1.3	-11.4	-11.4	-11.4
40522_at	X59834	1170	Human rearranged mRNA for glutamine synthase.	-1.9	1.2	1.2	-1.5
32696_at	X59841	1171	Human PBX3 mRNA.	5.1	4.5	1.0	1.0
38121_at	X59892	1172	H.sapiens mRNA for IFN-inducible gamma2 protein.	-1.0	-10.5	-1.5	-10.5
1768_s_at	X59932	1173	H.sapiens cyl mRNA for cytoplasmic tyrosine kinase.	-1.8	-2.3	-2.8	-2.3
37675_at	X60036	1174	H.sapiens mRNA for mitochondrial phosphate carrier protein.	-2.6	-1.9	-2.2	-1.7
1000_at	X60188	1175	Human ERK1 mRNA for protein serine/threonine kinase.	1.0	1.0	-2.6	-1.6
37285_at	X60364	1176	Human ALAS mRNA for 5-aminolevulinate synthase precursor.	-1.2	2.7	2.0	2.4
38566_at	X60382	1177	H.sapiens COL10A1 gene for collagen (alpha-1 type X).	2.4	3.7	1.2	2.6
32184_at	X61118	1178	Human TTG-2 mRNA for a cysteine rich protein with LIM motif.	-2.1	-4.6	-1.3	1.3
37294_at	X61123	1179	Human BTG1 mRNA.	-1.2	1.0	-2.4	-2.2
40362_at	X61498	1180	H.sapiens mRNA for NF-kB subunit.	2.4	14.4	11.2	12.3
36902_at	X61587	1181	H.sapiens rhoG mRNA for GTPase.	-2.5	-3.8	-2.3	-2.0
794_at	X62055	1182	H.sapiens PTP1C mRNA for protein-tyrosine phosphatase 1C.	-2.1	-2.8	-2.9	-1.7
38065_at	X62534	1183	H.sapiens HMG-2 mRNA.	-4.2	-24.3	-3.3	-7.2
37003_at	X62654	1184	H.sapiens gene for Me491/CD63 antigen.	1.4	2.8	4.8	4.3
32318_s_at	X63432	1185	H.sapiens ACTB mRNA for mutant beta-actin (beta'-actin).	3.1	3.2	-1.2	2.6
32435_at	X63527	1186	H.sapiens mRNA for ribosomal protein L19.	-1.7	-1.5	-1.6	-1.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
40791_at	X63564	1187	H.sapiens mRNA for RNA polymerase II largest subunit.	-5.2	-1.9	-1.8	-1.9
39097_at	X63753	1188	H.sapiens son-a mRNA.	-1.9	-1.0	-2.6	-2.9
40768_s_at	X64228	1189	H.sapiens can mRNA.	-2.0	-9.0	-47.7	-47.7
37544_at	X64318	1190	H.sapiens E4BP4 gene.	2.2	2.6	2.6	2.5
36162_at	X64364	1191	H.sapiens mRNA for M6 antigen.	1.4	-1.1	-2.0	-1.4
31509_at	X64707	1192	H.sapiens BBC1 mRNA.	1.6	-19.2	-1.2	-1.3
31775_at	X65018	1193	H.sapiens mRNA for lung surfactant protein D.	1.8	3.8	1.8	4.5
31673_s_at	X65784	1194	H.sapiens CAR gene.	-1.6	-1.5	-1.4	-2.7
33467_at	X66171	1195	H.sapiens CMRF35 mRNA, complete CDS.	-8.9	3.4	2.2	5.6
1225_g_at	X66363	1196	H.sapiens mRNA PCTAIRE-1 for serine/threonine protein kinase.	-2.4	9.9	2.9	2.3
421_at	X66397	1197	H.sapiens tpr mRNA.	-5.5	1.3	-1.5	-1.3
422_s_at	X66867	1198	Human helix-loop-helix zipper protein (max) mRNA, complete cds.	-1.0	-1.8	-1.4	-1.3
423_at	X66899	1199	H.sapiens EWS mRNA.	-4.4	-19.1	-1.4	-1.1
40593_at	X66975	1200	H.sapiens mRNA for heterogeneous nuclear ribonucleoprotein.	3.1	-2.3	-3.1	-2.4
31583_at	X67247	1201	H.sapiens rpS8 gene for ribosomal protein S8.	1.8	-2.8	-2.2	-2.0
35125_at	X67309	1202	H.sapiens gene for ribosomal protein S6.	-1.1	-1.9	-1.7	-1.5
37689_s_at	X68090	1203	H.sapiens Fc-gamma-RIIA gene for IgG Fc receptor class IIA (5'flank).	-3.4	1.0	-1.0	-4.2
1005_at	X68277	1204	H.sapiens CL 100 mRNA for protein tyrosine phosphatase.	4.0	4.2	2.2	-1.2
41573_at	X68560	1205	H.sapiens SPR-2 mRNA for GT box binding protein.	-1.5	-1.1	-1.2	-1.1
31952_at	X69391	1206	H.sapiens mRNA for ribosomal protein L6.	-1.8	1.6	-1.7	1.0
1984_s_at	X69549	1207	Human GDP-dissociation inhibitor protein (Ly-GDI) mRNA, complete cds.	1.0	-2.5	-1.3	-8.1
40164_at	X69550	1208	H.sapiens mRNA for rho GDP-dissociation Inhibitor 1.	2.9	7.0	6.8	6.9
38076_at	X69907	1210	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).	1.6	2.2	-1.7	1.9
32529_at	X69910	1211	H.sapiens p63 mRNA for transmembrane protein.	1.7	5.8	2.8	3.5
37994_at	X69962	1212	H.sapiens FMR-1 mRNA.	-1.7	-2.6	-3.8	-1.4
382_at	X70218	1213	Homo sapiens mRNA for protein phosphatase X.	-3.3	-2.0	-2.3	-2.4
36174_at	X70326	1214	H.sapiens MacMarcks mRNA.	-1.3	4.7	1.9	2.2
35175_f_at	X70940	1215	H.sapiens mRNA for elongation factor 1 alpha-2.	2.9	13.2	6.1	12.8
35174_i_at	X70940	1215	H.sapiens mRNA for elongation factor 1 alpha-2.	2.9	-1.1	-3.7	-1.5
35966_at	X71125	1216	H.sapiens mRNA for glutamine cyclotransferase.	-1.5	-1.9	-2.8	-1.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38686_at	X71490	1217	H.sapiens mRNA for vacuolar proton ATPase, subunit D.	-1.1	1.7	1.8	1.8
384_at	X71874	1218	#N/A	-1.7	-1.5	-4.1	-2.7
33931_at	X71973	1219	H.sapiens GPx-4 mRNA for phospholipid hydroperoxide glutathione peroxidase.	-1.7	-6.7	-2.3	-1.8
39415_at	X72727	1221	H.sapiens tunp mRNA for transformation upregulated nuclear protein.	-1.5	-1.4	-1.5	-3.1
40961_at	X72889	1222	H.sapiens hbrm mRNA.	1.7	-2.0	-1.2	-2.2
34005_at	X73079	1223	Homo sapiens encoding Polymeric immunoglobulin receptor.	1.0	6.5	1.3	4.7
40502_r_at	X73114	1224	H.sapiens mRNA for slow MyBP-C.	5.2	1.0	1.0	5.7
37725_at	X74008	1225	H.sapiens mRNA for protein phosphatase 1 gamma.	2.5	-2.6	-3.6	-2.9
36147_at	X74104	1226	H.sapiens mRNA for TRAP beta subunit.	1.1	-1.1	1.4	-2.1
36375_at	X74614	1227	H.sapiens ODF2 (allele 2) gene for outer dense fiber protein.	2.4	1.3	1.3	1.2
36180_s_at	X75346	1228	H.sapiens mRNA for MAP kinase activated protein kinase.	1.0	7.3	4.9	5.2
1439_s_at	X75346	1228	Human MAP kinase activated protein kinase 2 mRNA, complete cds.	1.0	13.9	10.3	9.4
33988_at	X75861	1229	H.sapiens TEGT gene.	1.1	-1.7	-1.6	-1.5
33368_at	X76040	1230	H.sapiens mRNA for Lon protease-like protein.	5.0	4.5	5.1	2.5
32597_at	X76061	1231	H.sapiens p130 mRNA for 130K protein.	-3.0	-1.2	-1.9	-1.5
36199_at	X76105	1232	H.sapiens DAP-1 mRNA.	-1.5	-1.6	-1.2	-2.1
37367_at	X76228	1233	H.sapiens mRNA for vacuolar H+ ATPase E subunit.	-2.0	1.1	1.1	1.4
34311_at	X76648	1234	H.sapiens mRNA for glutaredoxin.	-3.8	-3.6	-9.0	-6.1
34855_at	X76770	1235	H.sapiens PAP mRNA.	1.2	2.0	-1.3	-2.2
38895_i_at	X77094	1236	H.sapiens mRNA for p40phox.	-1.0	-2.5	-4.6	-2.2
38403_at	X77196	1237	H.sapiens mRNA for lysosome-associated membrane protein-2.	-4.6	-1.5	-1.7	-2.5
33867_s_at	X77494	1238	H.sapiens MSSP-2 mRNA.	1.1	-19.7	-5.0	-4.7
39174_at	X77548	1239	H. sapiens cDNA for RFG.	-1.2	-3.6	-6.3	-8.0
35746_r_at	X78136	1240	H.sapiens hnRNP-E2 mRNA.	-1.7	1.3	-1.1	-1.4
35745_f_at	X78136	1240	H.sapiens hnRNP-E2 mRNA.	-1.7	-1.1	-1.7	-1.1
31804_f_at	X78283	1241	H.sapiens mRNA for aryl sulfotransferase (ST1A3).	-1.4	-3.2	-3.6	-3.9
38130_s_at	X78711	1242	H.sapiens mRNA for glycerol kinase testis specific 1.	-2.5	5.4	7.1	3.9
39649_at	X78817	1243	H.sapiens partial C1 mRNA.	1.2	-2.2	-1.9	-2.0
34544_at	X78925	1244	H.sapiens HZF2 mRNA for zinc finger protein.	1.7	12.9	17.0	10.2
32588_s_at	X78992	1245	H.sapiens ERF-2 mRNA.	-137.4	-8.6	-8.3	-3.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
38740_at	X79067	1246	H.sapiens ERF-1 mRNA 3' end.	2.3	3.2	1.6	1.8
31872_at	X79201	1247	H.sapiens mRNA for SYT.	1.0	8.0	-1.2	1.6
36142_at	X79204	1248	H.sapiens SCA1 mRNA for ataxin.	-3.3	-7.0	-7.0	-7.0
41178_at	X79234	1249	H.sapiens mRNA for ribosomal protein L11.	-1.3	-1.7	-1.9	-2.3
36152_at	X79353	1250	H.sapiens XAP-4 mRNA for GDP-dissociation inhibitor.	-1.6	1.2	-1.3	1.2
38014_at	X79448	1251	H.sapiens IFI-4 mRNA for type I protein.	-1.3	-3.5	-5.0	-4.2
38064_at	X79882	1252	H.sapiens lrp mRNA.	-2.1	-2.9	-2.5	-2.6
38437_at	X80199	1253	H.sapiens MLN51 mRNA.	-2.0	-2.7	-2.8	-1.9
36480_at	X80497	1254	H.sapiens PHKLA mRNA.	-1.1	-1.9	-4.1	-3.4
39774_at	X80695	1255	H.sapiens OXA1Hs mRNA.	-1.7	-1.7	-1.6	1.4
40912_s_at	X81372	1257	H.sapiens mRNA for biphenyl hydrolase-related protein.	11.1	13.5	3.0	3.4
32964_at	X81479	1258	H.sapiens mRNA for EMR1 hormone receptor.	-3.5	-1.3	1.0	-1.1
39308_r_at	X81637	1259	H.sapiens clathrin light chain b gene.	-4.0	3.7	-1.3	-1.1
39307_s_at	X81637	1259	H.sapiens clathrin light chain b gene.	-4.0	1.2	-4.2	-4.2
41724_at	X81817	1260	H.sapiens BAP31 mRNA.	-1.4	-7.7	-1.7	-1.8
36825_at	X82200	1261	H.sapiens Staf50 mRNA.	-2.7	-4.4	-2.3	-1.6
36181_at	X82456	1262	H.sapiens MLN50 mRNA.	-2.1	-3.6	-3.2	-2.7
37029_at	X83218	1263	H.sapiens mRNA for ATP synthase.	2.1	-5.2	-5.2	-5.2
1440_s_at	X83490	1264	H.sapiens mRNA for APO-1 cell surface antigen.	-1.2	2.9	-1.8	-3.7
34469_at	X84746	1265	H.sapiens Histo-blood group AB0 gene, exon 1.	10.0	7.0	4.1	4.7
34733_at	X85237	1266	H.sapiens mRNA for splicing factor SF3a120.	1.9	-1.2	1.1	-1.1
36137_at	X86691	1267	H.sapiens mRNA for 218kD Mi-2 protein.	1.2	1.9	1.2	1.6
133_at	X87212	1268	H.sapiens mRNA for cathepsin C.	-10.7	-1.0	-1.4	1.2
38464_at	X87237	1269	H.sapiens mRNA for processing a-glucosidase I.	10.0	1.0	1.0	1.0
41184_s_at	X87344	1270	#N/A	-3.3	-2.1	-23.4	-23.4
40777_at	X87838	1271	H.sapiens mRNA for beta-catenin.	1.8	-1.3	-1.4	-3.0
36614_at	X87949	1272	H.sapiens mRNA for BiP protein.	1.4	-1.1	-1.0	-2.9
36984_f_at	X89214	1273	H.sapiens mRNA for haptoglobin related protein.	1.8	-2.9	-1.0	1.4
391_at	X89416	1274	H.sapiens mRNA for protein phosphatase 5.	4.6	-1.3	2.7	-1.3
392_g_at	X89416	1274	H.sapiens mRNA for protein phosphatase 5.	4.6	-2.0	4.6	5.5

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37089_at	X89654	1275	H.sapiens mRNA for cyritestin protein (clone T4A).	8.7	1.0	1.0	1.0
37351_at	X90858	1276	H.sapiens mRNA for uridine phosphorylase.	1.3	6.6	2.4	-3.9
31558_at	X91103	1277	H.sapiens mRNA for Hr44 protein.	2.5	5.3	1.3	2.6
39425_at	X91247	1278	H.sapiens mRNA for thioredoxin reductase.	-5.1	1.4	1.2	1.5
34849_at	X91257	1279	H.sapiens mRNA for seryl-tRNA synthetase.	-10.2	1.9	-2.0	-1.4
34268_at	X91809	1280	H.sapiens mRNA for GAIP protein.	-2.4	-3.5	-4.5	-3.5
36972_at	X92098	1281	H.sapiens mRNA for transmembrane protein rnp24.	1.9	-1.4	-1.7	-1.6
34753_at	X92396	1282	H.sapiens mRNA for novel gene in Xq28 region.	1.4	-5.0	-2.1	-5.0
37188_at	X92720	1283	H.sapiens mRNA for phosphoenolpyruvate carboxykinase.	9.1	1.0	1.0	1.0
35625_at	X94630	1284	H.sapiens CD97 gene exon 1 (and joined CDS).	-2.4	-2.9	-3.6	-2.1
39342_at	X94754	1285	H.sapiens mRNA for yeast methionyl-tRNA synthetase homologue.	1.9	1.5	-1.4	-2.1
41051_at	X95073	1286	H.sapiens mRNA for translin associated protein X.	-1.0	-4.7	-1.9	-4.7
33659_at	X95404	1287	H.sapiens mRNA for non-muscle type cofilin.	1.0	2.1	1.3	1.4
39782_at	X95592	1288	H.sapiens mRNA for C1D protein.	-1.0	-2.1	-1.7	-6.7
36958_at	X95735	1289	Homo sapiens mRNA for zyxin.	1.3	1.9	-1.1	1.5
34669_at	X96717	1290	H.sapiens mRNA for transcription factor TFE3.	1.4	1.7	1.8	2.1
40698_at	X96719	1291	H.sapiens mRNA for AICL (activation-induced C-type lectin).	-2.1	-2.9	-1.6	-2.1
39347_at	X97074	1292	H.sapiens mRNS for clathrin-associated protein.	-2.1	-1.5	-3.5	-1.4
33425_at	X97548	1293	H.sapiens mRNA for TIF1beta zinc finger protein.	-2.4	-7.2	-2.0	1.2
33774_at	X98172	1294	H.sapiens mRNA for MACH-alpha-1 protein.	-20.7	-49.4	-7.5	-5.0
35997_g_at	X98261	1295	H.sapiens mRNA for M-phase phosphoprotein, mpp5.	1.8	2.3	1.9	4.8
35996_at	X98261	1295	H.sapiens mRNA for M-phase phosphoprotein, mpp5.	1.8	3.0	1.8	1.8
970_r_at	X98296	1296	H.sapiens mRNA for ubiquitin hydrolase.	-1.1	1.5	1.1	1.7
39159_at	X99656	1298	H.sapiens mRNA for protein containing SH3 domain, SH3GL1.	1.0	5.8	2.6	4.1
36709_at	Y00093	1300	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95.	2.0	1.7	1.1	1.7
39082_at	Y00097	1301	Human mRNA for protein p68.	3.3	2.0	1.2	1.3
33424_at	Y00281	1302	Human mRNA for ribophorin I.	-1.5	-6.3	-3.3	-8.1
972_s_at	Y00285	1303	Human cation-independent mannose 6-phosphate receptor mRNA, complete cds.	-1.6	-34.9	-13.0	-1.2
31950_at	Y00345	1304	Human mRNA for polyA binding protein.	1.1	1.6	1.7	1.6
37674_at	Y00451	1306	Human mRNA for 5-aminolevulinate synthase.	2.5	-5.0	-1.7	-1.6

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37177_at	Y00636	1307	Human mRNA for lymphocyte function associated antigen-3 (LFA-3).	-1.3	2.5	2.6	3.0
38547_at	Y00796	1308	Human mRNA for leukocyte-associated molecule-1 alpha subunit (LFA-1 alpha subunit).	-13.3	-14.2	-1.8	-2.8
35892_at	Y00816	1309	Human mRNA for complement receptor type 1 (CR1, C3b/C4b receptor, CD35).	1.4	-1.8	-1.4	1.9
41490_at	Y00971	1310	Human mRNA for phosphoriobosyl pyrophosphate synthetase subunit II (EC 2.7.6.1).	9.6	8.1	1.9	1.0
38331_at	Y07566	1311	H.sapiens mRNA for RIT protein.	-1.3	1.4	1.5	1.6
38479_at	Y07969	1312	H.sapiens mRNA for APRIL protein.	-1.3	2.2	-1.5	-2.9
32140_at	Y08110	1313	H.sapiens mRNA for mosaic protein LR11.	-1.1	-2.9	-3.0	-4.9
39950_at	Y08136	1314	H.sapiens mRNA for ASM-like phosphodiesterase 3a.	2.8	3.1	-1.9	-1.9
36197_at	Y08374	1315	H.sapiens gene encoding cartilage GP-39 protein, exon 1 and 2 (and joined CDS).	-1.2	-1.3	-1.3	-1.2
35228_at	Y08682	1316	H.sapiens mRNA for carnitine palmitoyltransferase I type I.	-3.5	-8.2	-8.2	-8.2
1300_at	Y08837	1317	Homo sapiens mRNA for RAD51-like protein (XRCC2).	1.0	5.1	2.5	3.3
38445_at	Y09160	1318	H.sapiens Sub1.5 mRNA.	-1.6	-5.0	-4.4	-6.2
32179_s_at	Y09568	1319	Homo sapiens mRNA for SNAP23B protein, complete CDS.	-1.9	1.2	-2.2	-2.2
381_s_at	Y10055	1321	H.sapiens mRNA for phosphoinositide 3-kinase.	1.3	1.3	-1.1	1.2
38642_at	Y10183	1322	H.sapiens mRNA for MEMD protein.	-2.0	2.1	-3.4	-3.4
37679_at	Y10313	1323	Homo sapiens mRNA for PC4 protein (IFRD1 gene).	-7.8	1.1	-2.5	-9.8
359_at	Y10659	1324	H.sapiens IL-13Ra mRNA.	-15.2	-1.2	-3.3	-1.9
35472_at	Y10745	1325	H.sapiens mRNA for inwardly rectifing potassium channel Kir4.2.	-1.3	1.1	1.3	-1.5
38862_at	Y11215	1326	Homo sapiens mRNA for SKAP55 protein.	1.8	2.7	-1.7	-1.0
40729_s_at	Y14768	1327	#N/A	-5.1	-7.2	-4.7	-2.0
33641_g_at	Y14768	1327	#N/A	-1.2	-2.7	-2.5	-3.1
36482_s_at	Y15724	1328	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS).	-2.1	-1.8	-2.8	-2.6
33822_at	Z11584	1329	H.sapiens mRNA for NuMA protein.	-7.4	1.1	-12.0	-12.0
976_s_at	Z11695	1330	H.sapiens 41kDa protein kinase related to rat ERK2.	-6.1	-1.3	-1.6	-1.3
32466_at	Z12962	1331	H.sapiens mRNA for homologue to yeast ribosomal protein L41.	-1.2	-1.2	-1.0	-1.2
362_at	Z15108	1332	H.sapiens mRNA for protein kinase C zeta.	-3.5	1.9	-1.6	-1.6
35121_at	Z18956	1333	H.sapiens mRNA for taurine transporter.	2.3	-1.2	1.2	1.9
34091_s_at	Z19554	1334	H.sapiens vimentin gene.	1.6	3.7	2.9	1.9

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
41256_at	Z21507	1335	H.sapiens EF-1delta gene encoding human elongation factor-1-delta.	1.5	-1.2	-1.4	-1.7
37645_at	Z22576	1336	H.sapiens CD69 gene.	3.7	11.9	3.9	-1.5
1615_at	Z23115	1337	H.sapiens bcl-xL mRNA.	-1.4	1.0	1.0	3.5
34742_at	Z23115	1337	H.sapiens bcl-xL mRNA.	-1.4	5.9	-2.8	1.5
34646_at	Z25749	1338	H.sapiens gene for ribosomal protein S7.	-4.4	-4.0	-1.7	-11.1
34085_at	Z26876	1339	H.sapiens gene for ribosomal protein L38.	1.1	-1.2	-1.3	-3.5
31505_at	Z28407	1340	H.sapiens mRNA for ribosomal protein L8.	-2.7	-2.1	-2.5	-2.5
37731_at	Z29064	1341	H.sapiens AF-1p mRNA.	-3.3	-4.6	-1.2	-4.6
34305_at	Z29505	1342	H.sapiens mRNA for nucleic acid binding protein sub2.3.	-2.1	-1.5	-1.6	-1.9
35646_at	Z35093	1343	H.sapiens mRNA for SURF-1.	-1.9	-1.8	-9.3	-1.8
36218_g_at	Z35102	1344	H.sapiens mRNA for Ndr protein kinase.	1.2	-2.2	-2.5	-1.8
36217_at	Z35102	1344	H.sapiens mRNA for Ndr protein kinase.	1.2	-8.9	-3.8	-8.9
37416_at	Z35227	1345	H.sapiens TTF mRNA for small G protein.	11.3	9.8	10.0	9.8
39591_s_at	Z36531	1346	H.sapiens mRNA for fibrinogen-like protein (pT49 protein).	-3.7	-4.5	-3.1	-4.2
39592_r_at	Z36531	1346	H.sapiens mRNA for fibrinogen-like protein (pT49 protein).	-3.7	-4.4	-3.3	-4.4
1925_at	Z36714	1347	H.sapiens mRNA for cyclin F.	1.0	18.8	9.2	10.6
35907_at	Z36714	1347	H.sapiens mRNA for cyclin F.	1.0	3.4	1.0	2.9
35292_at	Z37166	1348	H.sapiens BAT1 mRNA for nuclear RNA helicase (DEAD family).	-2.7	-1.4	-2.1	-2.5
36710_at	Z38026	1349	H.sapiens mRNA for FALL-39 peptide antibiotic.	-1.1	-1.5	-1.7	1.2
40964_at	Z46376	1350	H.sapiens HK2 mRNA for hexokinase II.	1.2	-1.2	-1.7	-3.2
39105_at	Z46389	1351	Homo sapiens encoding vasodilator-stimulated phosphoprotein (VASP).	-1.1	2.6	3.0	1.2
31951_s_at	Z48501	1352	H.sapiens mRNA for polyadenylate binding protein II.	-1.8	1.8	1.8	2.0
40142_at	Z48570	1353	H.sapiens Sp17 gene.	1.0	-1.9	1.1	6.1
31510_s_at	Z48950	1354	H.sapiens hH3.3B gene for histone H3.3.	1.4	1.1	1.9	-1.2
38091_at	Z49107	1355	H.sapiens mRNA for galectin.	-1.5	-1.2	-2.6	-1.5
33674_at	Z49148	1356	H.sapiens mRNA for ribosomal protein L29.	-1.6	-2.8	-2.5	-1.2
39003_at	Z50022	1357	H.sapiens mRNA for surface glycoprotein.	-3.7	-5.1	-3.7	-3.4
35909_at	Z50194	1358	H.sapiens mRNA for PQ-rich protein.	27.9	24.0	16.4	8.5
36630_at	Z50781	1359	H.sapiens mRNA for leucine zipper protein.	-1.7	-3.5	-8.8	-5.0
40784_at	Z69030	1360	H.sapiens mRNA for gamma 1 isoform of 61kDa regulatory subunit of PP2A.	-2.0	-1.4	-1.1	-1.7

Table 7. Genes identified by DNA chip analysis.

Affy ID	Genbank	Seq ID	Gene Bank Names	ratio E.coli	ratio KIM5	ratio KIM6	ratio yopH
37672_at	Z72499	1361	H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).	-1.1	-4.2	-1.3	-1.2
40466_at	Z74792	1362	H.sapiens mRNA for CCAAT transcription binding factor subunit gamma.	-1.3	-14.2	-3.0	-1.6
31523_f_at	Z80780	1364	H.sapiens H2B/h gene.	-1.0	-1.5	-2.2	-1.4
31524_f_at	Z80782	1365	H.sapiens H2B/k gene.	-1.0	-1.1	-1.1	1.0
39738_at	Z82215	1366	#N/A	-1.2	-2.7	-3.3	-2.3
39755_at	Z93930	1367	Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.	4.5	7.8	3.9	2.4
40771_at	Z98946	1368	Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane-organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence.	-1.4	-1.7	-1.7	-2.1
38713_at	Z99716	1369	#N/A	1.0	-1.1	1.2	2.0

Table 8. Genes identified by READS technology.

Affy ID	Genbank	Seq ID	Gene Symbol	Gene Name
35299_at	AB000409	15	MKNK1	MAP kinase-interacting serine/threonine kinase 1
34644_at	AB021288	29	B2M	Beta-2-microglobulin
37026_at	AF001461	39	COPEB	Core promoter element binding protein; CPBP
39043_at	AF006084	46	ARPC1B	Actin related protein 2/3 complex, subunit 1A (41 kD); p41-Arc
37024_at	AF010312	49	PIG7	LPS-induced TNF-alpha regulatory factor (LITAF)
34033_s_at	AF025531	57	LIR-7	Leukocyte immunoglobulin-like receptor 7
41198_at	AF055008	72	GRN	*Granulin*; *Epithelin*
35693_at	AF070616	75	HPCAL1	Hippocalcin-like 1; Calcium-binding protein BDR-1
40082_at	D10040	158	FACL1	Fatty-acid-Coenzyme A ligase, long-chain 1; Palmitoyl-CoA ligase
32434_at	D10522	160	MACS	Myristoylated alanine-rich protein kinase C substrate
40470_at	D10523	161	OGDH	Oxoglutarate dehydrogenase
1199_at	D13748	168	EIF4A1	Eukaryotic translation initiation factor 4A, isoform 1
1891_at	D14497	172	MAP3K8	MAP kinase kinase kinase 8
1891_at	D14497	172	MAP3K8	MAP kinase kinase kinase 8
41212_r_at	D26068	196	WBSCR1	Williams-Beuren syndrome chromosome region 1; KIAA0038; EIF-4H
40712_at	D26579	198	ADAM8	A disintegrin and metalloprotease domain 8; CD156
41237_at	D32129	220	HLA-A	
336_at	D38081	225	TBXA2R	Thromboxane A2 receptor
41632_at	D38550	228	E2F-3	E2F transcription factor 3; KIAA0075
38138_at	D38583	230	S100A11	S100 calcium-binding protein A11; Calgizzarin
38617_at	D45906	238	LIMK2	LIM domain kinase 2
1512_at	D86550	285	DYRK1A	DYRK dual specificity threonine kinase 1A
1622_at	D87116	297	PRKMK3	MAP kinase kinase 3b; MKK3b
36167_at	D89052	308	ATP6F	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD; Proton-ATPase-like protein yeast proteolipid (HATPL)
1426_at	D89077	309	SLA	Src-like-adapter
36675_r_at	J03191	329	PFN1	Profilin 1
1389_at	J03779	335	MME	Neprilysin; Enkephalinase; CD10
37200_at	J04162	340	CGR3A	Fc-gamma receptor, low affinity IIIa; CD16
676_g_at	J04164	341	IFI17	IFN-inducible protein 9-27; leu-13 antigen

Table 8. Genes identified by READS technology.

Affy ID	Genbank	Seq ID	Gene Symbol	Gene Name
1127_at	L07597	379	RPS6KA1	Ribosomal protein S6 kinase, 90kD, polypeptide 1
33146_at	L08246	382	MCL1	BCL2-related; Myeloid cell differentiation protein
37701_at	L13463	405	RGS2	Regulator of G-protein signaling 2, 24kD; G0S8
33943_at	L20941	424	FTH1	Ferritin, heavy polypeptide 1
37693_at	L40393	466	NUMB	Homologue of numb [Fruit fly]
37574_at	L43821	474	HEF1	Enhancer of filamentation 1
36669_at	L49169	478	FOSB	fosB; G0S3
1100_at	L76191	480	IRAK1	Interleukin 1 receptor-associated kinase 1
254_at	M11353	487	H3F3A	H3 histone, family 3A
37918_at	M15395	505	ITGB2	Integrin, beta 2; Mac-1 beta; LFA-1; CD18
35372_r_at	M17017	513	IL8	Interleukin 8
31557_at	M17733	514	TMSB4X	Thymosin, beta 4, X chromosome
35807_at	M21186	526	CYBA	p22-PHOX; Cytochrome b-245, alpha polypeptide
39385_at	M22324	529	ANPEP	Membrane alanyl aminopeptidase; CD13
245_at	M25280	541	SELL	Selectin L; Lymph node homing receptor; CD62L
2050_s_at	M29870	556	RAC1	Ras-related C3 botulinum toxin substrate 1
1372_at	M31165	560	TNFAIP6	TNF alpha-induced protein 6; Hyaluronate-binding protein
41038_at	M32011	566	NCF2	Neutrophil cytosolic factor 2; p67-PHOX
36889_at	M33195	569	FCER1G	Fc fragment of IgE, high affinity I
36493_at	M33552	575	LSP1	Lymphocyte-specific protein 1
37187_at	M36820	589	GRO2	GRO2 oncogene; MIP-2-alpha
38378_at	M37033	591	CD53	
2036_s_at	M59040	614	CD44	Hyaluronate receptor
40019_at	M60830	619	EVI2B	Ectropic viral integration site 2B; Intron of the neurofibromatosis type 1 (NF1) gene
36994_at	M62762	622	ATP6C	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD
36097_at	M62831	624	ETR101	Immediate early protein ETR101; ETR101 early response factor
1461_at	M69043	646	NFKBIA	I-kappa-B alpha
38326_at	M69199	647		Putative lymphocyte G0/G1 switch protein 2 (G0S2)
40840_at	M80254	655	PPIF	Cyclophilin F

Table 8. Genes identified by READS technology.

Affy ID	Genbank	Seq ID	Gene Symbol	Gene Name
37556_at	M81637	659	GCL	Grancalcin
35012_at	M81750	660	MNDA	Myeloid cell nuclear differentiation antigen
31330_at	M81757	661	RPS19	Ribosomal protein S19
38631_at	M92357	689	TNFAIP2	TNF alpha-induced protein 2; B94
40448_at	M92843	691	ZFP36	TTP; TIS11; G0S24
31508_at	S73591	726	VDUP1	Upregulated by 1,25-dihydroxyvitamin D-3; Homologue of HHCPA 78
853_at	S74017	727	NFE2L2	Nrf2
181_g_at	S82470	741		BB1; AN43 antigen
1061_at	U00672	746	IL10RA	Interleukin 10 receptor, alpha
33849_at	U02020	752	PBEF	Pre-B cell colony-enhancing factor; G0S9
36980_at	U03105	757	B4-2	B4-2 proline rich protein
41140_at	U05875	770	IFNGR2	Interferon-gamma receptor beta chain
32587_at	U07802	776	BRF2	EGF-response factor 2; Homologue of TIS11D [Mouse]
31432_g_at	U12255	797	FCGRT	Fc fragment of IgG, receptor, transporter, alpha
39319_at	U20158	830	LCP2	Lymphocyte cytosolic protein 2; SLP-76
2002_s_at	U27467	849	BCL2A1	BCL2-related protein A1; Bfl-1
36977_at	U39412	884	NAPA	Alpha-soluble NSF attachment protein (alpha SNAP)
840_at	U47742	919	ZNF220	Zinc finger protein 220; Monocytic leukaemia zinc finger protein (MOZ)
37360_at	U66711	974	LY6E	RIG-E; human homologue of LY6
36634_at	U72649	992	BTG2	TIS21; NGF-inducible PC3 anti-proliferative protein
41045_at	U77643	1002	SECTM1	Secreted and transmembrane 1
824_at	U90313	1037	GSTTLp28	Glutathione-S-transferase homologue
38276_at	U91616	1047	NFKBIE	I-kappa-B epsilon
1916_s_at	V01512	1059	FOS*	v-fos homologue; G0S7; c-fos
34160_at	X04098	1073	ACTG1	gamma-actin
39753_at	X06256	1083	ITGA5	Integrin alpha-5; Fibronectin receptor alpha subunit; CD49e
37328_at	X07743	1094	PLEK	Pleckstrin
41088_at	X12433	1096	HS1-2	Putative transmembrane protein
32316_s_at	X15183	1107	HSPCA	Heat shock 90kD protein 1, alpha
31584_at	X16064	1111	TPT1	IgE-dependent histamine-releasing factor

Table 8. Genes identified by READS technology.

Affy ID	Genbank	Seq ID	Gene Symbol	Gene Name
31820_at	X16663	1115	HCLS1	Hematopoietic cell-specific Lyn substrate 1; HS1
32227_at	X17042	1118	PRG1	Proteoglycan 1, secretory granule
789_at	X52541	1133	EGR1	G0S30; TIS8; KROX24; NGFIA; ETR103
38354_at	X52560	1134	CEBPB	NF-IL6; C/EBP beta
32321_at	X56841	1152	HLA-E	
38441_s_at	X59408	1166	MCP	Membrane cofactor protein; Trophoblast-lymphocyte cross-reactive antigen; CD46
402_s_at	X69819	1209	ICAM3	Intercellular adhesion molecule 3; CD50
39802_at	X72308	1220	SCYA7	Small inducible cytokine A7 (monocyte chemotactic protein 3)
33614_at	X80822	1256	RPL18A	Ribosomal protein L18a
35132_at	X98411	1297	MYO1E	Myosin IE
40518_at	Y00062	1299	PTPRC	Leukocyte common antigen; Protein tyrosine phosphatase, receptor type, c polypeptide; CD45
40637_at	Y00371	1305	HSPA10	Heat shock 70kD protein 10 (HSC71)
973_at	Y10032	1320	SGK	Serum/glucocorticoid regulated kinase
978_at	Z79581	1363	BCL6	B-cell CLL/lymphoma 6; Zinc finger protein 51

What is claimed is:

1. A method of detecting granulocyte activation, comprising:

(a) detecting the level of expression in a sample of one or more genes from Tables 2-8;

(b) comparing the expression level to an expression level in an un-activated granulocyte, wherein differential expression of the genes in Tables 2-8 is indicative of granulocyte activation.

2. A method of modulating granulocyte activation, comprising:

(a) contacting a granulocyte with an agent, wherein the agent alters the expression of at least one gene in Tables 2-8 thereby modulating granulocyte activation.

3. A method of screening for an agent capable of modulating granulocyte activation, comprising:

(a) preparing a first gene expression profile of a cell population comprising granulocytes, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) exposing the cell population to the agent;

(c) preparing second gene expression profile of the agent-exposed cell population; and

(d) comparing the first and second gene expression profiles.

4. A method of detecting an inflamation in a tissue, comprising:

(a) detecting the level of expression in a sample of the tissue of one or more genes from Tables 2-8; wherein the level of expression of the genes in Tables 2-8 is indicative of inflammation.

5. A method of treating an inflammation in a tissue, comprising:

(a) contacting a tissue having an inflammation with an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the inflammation.

6. A method of screening for an agent capable of modulating an inflammation in a tissue, comprising:

(a) preparing a first gene expression profile of a sample of the tissue, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) exposing the tissue to the agent;

(c) preparing second gene expression profile of the agent-exposed tissue; and

(d) comparing the first and second gene expression profiles.

7. A method of detecting a chronic inflamation in a tissue, comprising:

(a) detecting the level of expression in a sample of the tissue of one or more genes from Tables 2-8; wherein the level of expression of the genes in Tables 2-8 is indicative of a chronic inflammation.

8. A method of treating a chronic inflammation in a tissue, comprising:

(a) contacting a tissue having a chronic inflammation with an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the chronic inflammation.

9. A method of screening for an agent capable of modulating a chronic inflammation in a tissue, comprising:

(a) preparing a first gene expression profile of a sample of the tissue, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) exposing the tissue to the agent;

(c) preparing a second gene expression profile of the agent-exposed tissue; and

(d) comparing the first and second gene expression profiles.

10. A method of detecting an allergic response in a subject, comprising:

(a) obtaining a sample from the subject, the sample comprising granulocytes;

(b) preparing a gene expression profile of the sample, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(c) comparing the expression level to an expression level in a sample from a normal individual, wherein differential expression of the genes in Tables 2-8 is indicative of an allergic response.

11. A method of treating an allergic response in a subject, comprising:

(a) administering to the subject an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the allergic response.

12. A method of screening for an agent capable of modulating an allergic response in a subject, comprising:

(a) preparing a first gene expression profile of a sample from the subject, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) administering to the subject an agent;

(c) preparing a second gene expression profile of a sample from the agent-exposed subject; and

(d) comparing the first and second gene expression profiles.

13. A method of detecting exposure of a subject to a pathogen, comprising:

(a) preparing a first gene expression profile of a granulocyte population from the subject, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) comparing the first gene expression profile to a second gene expression profile from a granulocyte population exposed to the pathogen and to a third gene expression profile from a granulocyte population not exposed to the pathogen; and

(c) determining whether the subject was exposed to the pathogen.

14. A method of treating a subject exposed to a pathogen, comprising:

(a) administering to the subject an agent, wherein the agent affects the expression of at least one gene in Tables 2-8 thereby treating the subject.

15. A method of screening for an agent that modulates a response of a granulocyte population to a pathogen, comprising:

(a) preparing a first gene expression profile of a first sample from the granulocyte population, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) exposing a second sample of the granulocyte population to a pathogen and preparing a second gene expression profile from the second sample;

(c) contacting the pathogen-exposed granulocyte population with an agent and preparing a third gene expression profile from the agent-contacted pathogen-exposed population;

(d) comparing the first, second and third gene expression profiles; and

(e) identifying agents that modulate the response of a granulocyte population to the pathogen.

16. A method of detecting a sterile inflammatory disease in a subject, comprising:

(a) detecting the level of expression in a sample from the subject of one or more genes from Tables 2-8; wherein the level of expression of the genes in Tables 2-8 is indicative of a sterile inflammatory disease.

17. A method of treating a sterile inflammatory disease in a subject, comprising:

(a) contacting the subject with an agent, wherein the agent alters the expression in the tissue of at least one gene in Tables 2-8 thereby treating the sterile inflammatory disease.

18. A method of screening for an agent capable of modulating a sterile inflammatory disease in a subject, comprising:

(a) preparing a first gene expression profile of a sample from the subject, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;

(b) exposing the subject to the agent;

(c) preparing second gene expression profile of a sample obtained from the

agent-exposed subject; and

(d) comparing the first and second gene expression profiles.

19. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

20. A composition according to claim 19, wherein the composition comprises at least 3 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

21. A composition according to claim 19, wherein the composition comprises at least 5 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

22. A composition according to claim 19, wherein the composition comprises at least 7 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

23. A composition according to claim 19, wherein the composition comprises at least 10 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

24. A composition according to any one of claims 19-23, wherein at least one oligonucleotide is attached to a solid support.

25. A composition according to claim 24, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

26. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

27. A solid support according to claim 26, wherein at least one of the oligonucleotides is covalently attached to the solid support.

28. A solid support according to claim 26, wherein at least one of the oligonucleotides is non-covalently attached to the solid support.

29. A solid support according to claim 26, wherein the support comprises at least 10 different oligonucleotides in discrete locations per square centimeter.

30. A solid support according to claim 26, wherein the support comprises at least 100 different oligonucleotides in discrete locations per square centimeter.

31. A solid support according to claim 26, wherein the support comprises at least 1000 different oligonucleotides in discrete locations per square centimeter.

32. A solid support according to claim 26, wherein the support comprises at least 10,000 different oligonucleotides in discrete locations per square centimeter.

33. A computer system comprising:

(a) a database containing information identifying an expression level in a cell population comprising granulocytes of a set of genes comprising at least two genes in Tables 2-8; and

(b) a user interface to view the information.

34. A computer system of claim 33, wherein the database further comprises sequence information for the genes.

35. A computer system of claim 33, wherein the database further comprises information identifying the expression level for the set of genes in a cell population comprising non-activated granulocytes.

36. A computer system of claim 33, wherein the database further comprises information identifying the expression level of the set of genes in a cell population comprising activated granulocytes.

37. A computer system of any of claims 33-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

38. A computer system of claim 37, wherein the external database is GenBank.

39. A method of using a computer system of any one of claims 33-36 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 2-8, comprising:

(a) comparing the expression level of at least one gene in Tables 2-8 in the tissue or cell to the level of expression of the gene in the database.

40. A method of claim 39, wherein the expression level of at least two genes are compared.

41. A method of claim 39, wherein the expression level of at least five genes are compared.

42. A method of claim 39, wherein the expression level of at least ten genes are compared.

43. A method of claim 39, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in a cell population comprising activated granulocytes.

44. A method of identifying virulence factor genes in a pathogen, comprising:

(a) preparing a first gene expression profile of a quiescent granulocyte population;

(b) preparing a second gene expression profile of a granulocyte population

exposed to a virulent or avirulent strain of pathogen;

(c) preparing a third gene expression profile from a granulocyte population exposed to a strain of pathogen with a mutation in a putative virulence factor gene; and

(d) comparing the first, second and third gene expression profiles to identify a virulence factor gene of the pathogen.

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WO 02/028999 A3

(54) Title: GENE EXPRESSION PROFILES IN GRANULOCYTIC CELLS

(57) Abstract: The present invention identifies the global changes in gene expression associated with activation of granulocytes. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/30821

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : G01N 33/48
US CL : 702/19

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 702/19

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EAST, STN

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Winzen et al. The p38 MAP Kinase Pathway Signals for Cytokine-induced mRNA Stabilization via MAP Kinase-activated protein kinase 2 and an AU-rich region-targeted mechanism. The EMBO Journal. 1999, Vol. 18, No. 18, pages 4969-4980.	1, 4, 7, 10, and 16
A	Cao et al. Expression of Plasma Platelet-activating Factor Acetylhydrolase is Transcriptionally Regulated by Mediators of Inflammation. The Journal of Biological Chemistry. 13 February 1998, Vol. 273, No. 7, pages 4012-4020.	1, 4, 7, 10, and 16

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
07 April 2002 (07.04.2002)	12 JUN 2002
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Shubo "Joe" Zhou Telephone No. (703)-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/30821

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1, 4, 7, 10 and 16

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group 1 (claim(s) 1, 4, 7, 10, and 16), drawn to a method for detection involving the expression of one or more genes in Tables 2-8.

Group 2 (claim(s) 2), drawn to a method for modulating granulocyte activation involving the expression of one or more genes in Tables 2-8.

Group 3 (claim(s) 3, 6, 9, 12-13, and 18), drawn to method of screening, involving the expression of one or more genes in Tables 2-8.

Group 4 (claim(s) 5 and 8), drawn to methods of treating, involving the expression of one or more genes in Tables 2-8.

Group 5 (claim(s) 11), drawn to method of treating an allergic response in a subject involving altering the expression of one or more genes in Tables 2-8.

Group 6 (claim(s) 14), drawn to a method of treating a subject exposed to a phathogen involving affecting the expression of one or more genes in Tables 2-8.

Group 7 (claim(s) 15), drawn to a method of screening for an agent that modulate a response of a granulocyte to a pathogen involving the expression of one or more genes in Tables 2-8.

Group 8 (claim(s) 17), drawn to a method of treating a sterile inflammatory disease in a subject involving detecting the expression of one or more genes in Tables 2-8.

Group 9 (claim(s) 19-25), drawn to composition comprising oligonucleotides hybridizing to more or more genes in Tables 2-8.

Group 10 (claim(s) 26-32), drawn to solid support comprising oligonucleotides hybridizing to one or more genes in Tables 2-8.

Group 11 (claim(s) 33-43), drawn to computer systems comprising a database comprising the one or more genes in Tables 2-8.

Group 12(claim(s) 44), drawn to a method for identifying virulence factor genes in a pathoge.

The inventions listed as Groups 1-12 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reason:

The methods or composition or computer systems are unrelated, each to each other. The one or more genes in Tables 2-8 are not novel because they are all from GenBank database. Thus, the technical feature of the

polynucleotide sequence is not special and the groups are not so linked under PCT Rule 13.1. Additionally the claimed methods require different reagents, procedures and produce different results which are not coextensive and which do not share the same technical feature.

Thus, in summary, the inventions listed as Groups 1-12 are not so linked under PCT Rule 13.1.